

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 1, 2005, 18:05:25 ; Search time 109.109 Seconds  
(without alignments)  
3214.888 Million cell updates/sec

Title: US-09-591-632-2

Perfect score: 3594

Sequence: 1 MSDSNQNNQNYQYQSQNG.....FTLRDQGTIAIGKIVKIAE 685

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3594	100.0	685	1 ERF2_YEAST	P05453 saccharomyc
2	3590	99.9	685	2 Q9HGV1	Q9HGV1 saccharomyc
3	3587	99.8	685	2 Q8TFB8	Q8TFB8 saccharomyc
4	3455.5	96.1	666	2 Q8TFR7	Q8TFR7 saccharomyc
5	3450.5	96.0	666	2 Q8TFR8	Q8TFR8 saccharomyc
6	2632.5	73.2	688	2 Q8FVM2	Q8FVM2 candida gla
7	2549.5	70.9	662	2 Q9HG14	Q9HG14 zygosacchar
8	2471	68.8	700	2 Q6CQF8	Q6CQF8 kluyveromyc
9	2471	68.8	700	2 Q9HG18	Q9HG18 kluyveromyc
10	2464	68.6	691	2 Q750T4	Q750T4 ashbya goss
11	2367	65.9	712	2 Q9HG17	Q9HG17 candida mal
12	2345.5	65.3	715	1 ERF2_CANAL	Q13354 candida alb
13	2303	64.1	435	2 Q6Q7I3	Q6Q7I3 saccharomyc
14	2296	63.9	435	2 Q6Q7I6	Q6Q7I6 saccharomyc
15	2287	63.6	435	2 Q6Q7I2	Q6Q7I2 saccharomyc
16	2283.5	63.5	701	2 Q9HG16	Q9HG16 debaryomyc
17	2281	63.5	435	2 Q6Q7I4	Q6Q7I4 saccharomyc
18	2277.5	63.4	701	2 Q6BQW4	Q6BQW4 debaryomyc
19	2274	63.3	429	2 Q9BUJ2	Q9BUJ2 saccharomyc
20	2272	63.2	435	2 Q6Q7I1	Q6Q7I1 saccharomyc
21	2267	63.1	429	2 Q96TJ4	Q96TJ4 saccharomyc
22	2263	63.0	429	2 Q96UI9	Q96UI9 saccharomyc
23	2257	62.8	429	2 Q96UI1	Q96UI1 saccharomyc
24	2253	62.7	429	2 Q96UU0	Q96UU0 saccharomyc
25	2249	62.6	429	2 Q96UI8	Q96UI8 saccharomyc
26	2243	62.4	429	2 Q96TQ9	Q96TQ9 saccharomyc
27	2178	60.6	434	2 Q96UJ3	Q96UJ3 saccharomyc
28	2177	60.6	741	1 ERF2_PICPI	P23637 pichia pinu
29	1877	52.2	742	2 Q9HG15	Q9HG15 yarrowia li
30	1855	51.6	728	2 Q6CFC9	Q6CFC9 yarrowia li
31	1721	47.9	730	2 Q7S6P5	Q7S6P5 neurospora

#### RESULT 1

ID	ERF2_YEAST	STANDARD;	PRT;	685 AA.
AC	P05453; P05420;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Eukaryotic peptide chain release factor GTP-binding subunit (ERF2)			
DE	(Translation release factor 3) (ERF3) (ERF-3) (Omnipotent suppressor protein 2) (G1 to S phase transition protein 1).			
DE	Name=SUP35; Synonyms=GST1, PNM2, SAL3, SUP12, SUP2;			
GN	OrderedLocustNames=YDR172W; ORFNames=YD9395.05;			
OS	Saccharomyces cerevisiae (Baker's Yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.			
OX	NCBI_TaxID=4932;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88329727; PubMed=3047009; DOI=10.1016/0378-1119(88)90223-5;			
RA	Kushnirov V.V., Ter-Avanesyan M.D., Telckov M.V., Surguchov A.P.,			
RA	Smirnov V.N., Inge-Vechtomov S.G.;			
RT	"Nucleotide sequence of the SUP2 (SUP35) gene of Saccharomycetes cerevisiae."			
RT	Gene 66:45-54(1988).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=87213095; PubMed=3556215; DOI=10.1016/0014-5793(87)80157-6;			
RX	Kushnirov V.V., Ter-Avanesyan M.D., Surguchov A.P., Smirnov V.N.,			
RA	Inge-Vechtomov S.G.;			
RT	"Localization of possible functional domains in sup2 gene product of the yeast Saccharomycetes cerevisiae."			
RT	FEBS Lett. 215:257-260(1987).			
RL	[3]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=88172503; PubMed=3280807;			
RX	Wilson P.G., Culbertson M.N.;			
RA	"SUP12 suppressor protein of yeast. A fusion protein related to the EF-1 family of elongation factors."			
RT	J. Mol. Biol. 199:559-573(1988).			
RL	[4]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=88296422; PubMed=2841115;			
RX	Kukuchi Y., Shinatake H., Kikuchi A.;			
RA	"A yeast gene required for the G1-to-S transition encodes a protein containing an A-kinase target site and GTPase domain."			
RT	EMBO J. 7:1175-1182(1988).			
RL	[5]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=S288c / AB972;			
RX	MEDLINE=97313263; PubMed=9169867;			
RA	Jacq C., Alt-Moerbe J., Andre B., Arnold W., Ballestra J.P.G.,			
RA	Bargues M., Baron L., Becker A., Biteau N., Bloeker H., Blugeon C.,			
RA	Boskovic J., Brandt P., Brueckner M., Buitrage M.J., Cosser F.,			
RA	Delaveau T., del Rey F., Dujon B., Eide L.G., Garcia-Cantalejo J.M.,			

32	1714	47.7	716	2	O42787	O42787 podospora a
33	1689	47.0	662	1	ERF2_SCHPO	O74718 schizosacch
34	1626	45.2	629	2	Q96WS7	Q96WS7 pneumocysti
35	1377	38.3	633	2	Q96GF2	Q96GF2 homo sapien
36	1375	38.3	614	2	Q91855	Q91855 xenopus lae
37	1364	38.0	498	2	O7KZX8	O7KZX8 homo sapien
38	1359.5	37.8	553	2	O6DD07	O6DD07 xenopus lae
39	1357	37.8	587	2	Q8K2E1	Q8K2E1 mus musculu
40	1354.5	37.7	499	1	GSP1_HUMAN	P15170 homo sapien
41	1353.5	37.7	588	2	Q9N2G7	Q9N2G7 oryctolagus
42	1353.5	37.7	636	2	Q6AYD5	Q6AYD5 rattus norv
43	1352	37.6	498	2	O8CCV1	O8CCV1 mus musculu
44	1346.5	37.5	597	2	O88180	O88180 mus musculu
45	1346.5	37.5	628	2	Q9NY44	Q9NY44 homo sapien

#### ALIGNMENTS





```
QY 301 DAGRQGYLSWVMDTNKEERNDGKTIIEVGKAYFETEKRRYTIILDAPGHKMYVSEMIIGAS 360
DB 301 DAGRQGYLSWVMDTNKEERNDGKTIIEVGKAYFETEKRRYTIILDAPGHKMYVSEMIIGAS 360
QY 361 QADVGVLVISARKGEYETGFERGGQTRHALLAKTQGVNKMVWVVKMDPTVNSKERY 420
DB 361 QADVGVLVISARKGEYETGFERGGQTRHALLAKTQGVNKMVWVVKMDPTVNSKERY 420
QY 421 DQCVSNVSNFLRAIGYNIKTDDVMPVSGYSGANLKDHDVDPKPCPWTGPTLLEYLDTMN 480
DB 421 DQCVSNVSNFLRAIGYNIKTDDVMPVSGYSGANLKDHDVDPKPCPWTGPTLLEYLDTMN 480
QY 481 HVDRHINAPFMLPTAAKMKDLGTTVEGKIESGHIKKGSTLLMPNKTAVEIQNIYNEN 540
DB 481 HVDRHINAPFMLPTAAKMKDLGTTVEGKIESGHIKKGSTLLMPNKTAVEIQNIYNEN 540
QY 541 EVDNMCGEQVKLRIGVEBEDISPGFVLTSPPKPIKSVTKFVAQIAIIVELKSIIAAGFS 600
DB 541 EVDNMCGEQVKLRIGVEBEDISPGFVLTSPPKPIKSVTKFVAQIAIIVELKSIIAAGFS 600
QY 601 CVMHVHTAIEBVHIVKLLHLEKGTNRKSKPPAFKGMKVIIVLETPAPVCVETQDY 660
DB 601 CVMHVHTAIEBVHIVKLLHLEKGTNRKSKPPAFKGMKVIIVLETPAPVCVETQDY 660
QY 661 POLGRFTLRDQGTIIAIGKIVKIAE 685
DB 661 POLGRFTLRDQGTIIAIGKIVKIAE 685

RESULT 4
Q8TRF7 ID Q8TRF7 PRELIMINARY; PRT; 666 AA.
AC Q8TRF7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Prion protein.
GN Name=SUP35;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCI4;
RX MEDLINE=22773310; PubMed=12890024;
RA Resende C.G., Outeiro T.F., Sands L., Lindquist S., Tuite M.F.;
RT "Prion protein gene polymorphisms in Saccharomyces cerevisiae.";
RL Mol. Microbiol. 49:1005-1017(2003).
DR GO; GO:0005255; F:GTP binding; IEA.
DR GO; GO:0003747; F:translation release factor activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0006415; P:translational termination; IEA.
DR InterPro; IPR004160; EFTU_Cterm.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR009001; Elong_init_C.
DR InterPro; IPR000795; ProtSyn_GTPbind.
DR InterPro; IPR009000; Translat factor.
DR InterPro; IPR003285; Yeast ERF.
DR Pfam; PF00009; GTP_EFTU_1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR Pfam; PF03143; GTP_EFTU_D3; 1.
DR PRINTS; PR00315; ELONGATNFCT.
DR PRINTS; PR01343; YEASTERF.
DR PROSITE; PS00301; EPACTOR_GTP; UNKNOWN 1.
KW GTP-binding; Prion; Protein biosynthesis.
SQ SEQUENCE 666 AA; 7408 MW; 13EA65612A0705F8 CRC64;
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Query Match 96.1%; Score 3455.5; DB 2; Length 666;  
Best Local Similarity 97.1%; Pred. No. 3.2e-168;  
Matches 665; Conservative 0; Mismatches 1; Indels 19; Gaps 1;

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QY 1 MSDSNOGNQNTQYQYSONGNOQGNRYQGYAYNAQAOPAGGYQNYQYSGYQGGY 60
DB 1 MSDSNOGNQNTQYQYSONGNOQGNRYQGYAYNAQAOPAGGYQNYQYSGYQGGY 60
QY 61 QQYNPDAGYQQYNPDAGYQQYNPDAGYQQYNPDAGYQQYNPDAGYQQYNPDAGY 120
DB 57 -----QGGYQQYNPDAGYQQYNPDAGYQQYNPDAGYQQYNPDAGYQQYNPDAGY 101
QY 121 SQGMSLNDFOKQKQAPKPKTKLKVSSSGIKLANATKKVGTGTPAESDKKEEKSAETK 180
DB 102 SQGMSLNDFOKQKQAPKPKTKLKVSSSGIKLANATKKVGTGTPAESDKKEEKSAETK 161
QY 181 EPTKEPTKVEEPKVEEPKVEEPKVEEPKVEEPKVEEPKVEEPKVEEPKVEEPK 240
DB 162 EPTKEPTKVEEPKVEEPKVEEPKVEEPKVEEPKVEEPKVEEPKVEEPKVEEPK 221
QY 241 EQEEVDVDEVDNMFQGHVSLIFMGHVDAGKSTMGNNLLYLTGSDKRTIEKYEREAK 300
DB 222 EQEEVDVDEVDNMFQGHVSLIFMGHVDAGKSTMGNNLLYLTGSDKRTIEKYEREAK 281
QY 301 DAGRQGYLSWVMDTNKEERNDGKTIIEVGKAYFETEKRRYTIILDAPGHKMYVSEMIIGAS 360
DB 282 DAGRQGYLSWVMDTNKEERNDGKTIIEVGKAYFETEKRRYTIILDAPGHKMYVSEMIIGAS 341
QY 361 QADVGVLVISARKGEYETGFERGGQTRHALLAKTQGVNKMVWVVKMDPTVNSKERY 420
DB 342 QADVGVLVISARKGEYETGFERGGQTRHALLAKTQGVNKMVWVVKMDPTVNSKERY 401
QY 421 DQCVSNVSNFLRAIGYNIKTDDVMPVSGYSGANLKDHDVDPKPCPWTGPTLLEYLDTMN 480
DB 402 DQCVSNVSNFLRAIGYNIKTDDVMPVSGYSGANLKDHDVDPKPCPWTGPTLLEYLDTMN 461
QY 481 HVDRHINAPFMLPTAAKMKDLGTTVEGKIESGHIKKGSTLLMPNKTAVEIQNIYNEN 540
DB 462 HVDRHINAPFMLPTAAKMKDLGTTVEGKIESGHIKKGSTLLMPNKTAVEIQNIYNEN 521
QY 541 EVDNMCGEQVKLRIGVEBEDISPGFVLTSPPKPIKSVTKFVAQIAIIVELKSIIAAGFS 600
DB 522 EVDNMCGEQVKLRIGVEBEDISPGFVLTSPPKPIKSVTKFVAQIAIIVELKSIIAAGFS 581
QY 601 CVMHVHTAIEBVHIVKLLHLEKGTNRKSKPPAFKGMKVIIVLETPAPVCVETQDY 660
DB 582 CVMHVHTAIEBVHIVKLLHLEKGTNRKSKPPAFKGMKVIIVLETPAPVCVETQDY 641
QY 661 POLGRFTLRDQGTIIAIGKIVKIAE 685
DB 642 POLGRFTLRDQGTIIAIGKIVKIAE 666

RESULT 5
Q8TRF8 ID Q8TRF8 PRELIMINARY; PRT; 666 AA.
AC Q8TRF8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Prion protein.
GN Name=SUP35;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCI3;
RX MEDLINE=22773310; PubMed=12890024;
RA Resende C.G., Outeiro T.F., Sands L., Lindquist S., Tuite M.F.;
RT "Prion protein gene polymorphisms in Saccharomyces cerevisiae.";
RL Mol. Microbiol. 49:1005-1017(2003).
DR EMBL; AY028646; AAK26177.1; -.
DR GO; GO:0005255; F:GTP binding; IEA.
DR GO; GO:0003747; F:translation release factor activity; IEA.
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QY 273 KSTWGGNLLYLTSVDRKRTIEKYBREAADAGROGWYLSWMDTNKEBRNDGKTIIEVGKAY 332
DB 276 KSTWGGNLLYLTSVDRKRTIEKYBREAADAGROGWYLSWMDTNKEBRNDGKTIIEVGKAY 335
QY 333 FETEKRRYTLIDAPGHKMYVSEMIIGGASQADVGVLVTSARKGEYETGFERGGQTRHALL 392
DB 336 FETEKRRYTLIDAPGHKMYVSEMIIGGASQADVGVLVTSARKGEYETGFERGGQTRHALL 395
QY 393 AKTOGVNKMVVVNMDDPTVNSKERYDQCVSNVSNFLRAIGHNIKTVDVFMVPSYSG 452
DB 396 AKTOGVNKMVVVNMDDPTVNSQERYDQCVSNLSNLYKAIGNVQDVVFMVPSYSG 455
QY 453 ANLKDHVDPKCEPNVGTPTLLELYLDTMNVHVRHINAPFPLPIAAKMDLGTIVGKTESG 512
DB 456 AGLKERVKECEPNVGTPTLLELYLDTMNVHVRHINAPFPLPIAAKMDLGTIVGKTESG 515
QY 513 HIKKGQSTLLMPNKTAVEIQNIYNETENEVDMAKMGQVQLRIKGVBEEDISPGFVLTS 572
DB 516 HIKKGQSTLLMPNKIPVEIQNIYNETENEVDMAKMGQVQLRIKGVBEEDISAGFVLTS 575
QY 573 KNPITSVTVFQAIAVELKSIIAAGFSCVMHVHTAIEEVHIVKLLHLEKGTNRKSKKP 632
DB 576 KNPITKNVTRFQAIAVELKSIINSAGFSCVMHVHTAIEEVHITRLHLKLRGTNRKSKKP 635
QY 633 PAFAKKGMKVIATLEAPVCVETQYDYPQLGRFLTRDQGTIIAGIKVIAE 685
DB 636 PAFAKKGMKIIATLEAPVCVETQYDYPQLGRFLTRDQGTIIAGIKVILE 688

RESULT 7
Q9HG14 PRELIMINARY; PRT; 662 AA.
ID Q9HG14
AC Q9HG14;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polypeptide release factor 3.
GN Name=sup35;
OS Zygosaccharomyces rouxii (Candida mogii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.
OX NCBI_TaxID=4956;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21324710; PubMed=11430816; DOI=10.1016/S1097-2765(01)00259-3;
RA Nakayashiki T., Ebihara K., Bannai H., Nakamura Y.;
RT "Yeast [PSI+] 'prions' that are crosstransmissible and susceptible
RL beyond a species barrier through a quasi-prion state.";
RL Mol. Cell 7:1121-1130(2001).
DR EMBL; AB039753; BAB12684.2; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003747; F:translation release factor activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0006415; P:translational termination; IEA.
DR InterPro; IPR004160; EFTU_Cterm.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR009001; Elong_init_C.
DR InterPro; IPR000795; ProtSyn_GTPbind.
DR InterPro; IPR009000; Translat_factor.
DR InterPro; IPR003285; Yeast_ERF.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR Pfam; PF03143; GTP_EFTU_D3; 1.
DR PRINTS; PR00315; ELONGATNFCT.
DR PRINTS; PR01343; YEASTERF.
DR PROSITE; PS00301; EFACITOR_GTP; UNKNOWN_1.
KW GTP-binding; Protein biosynthesis.
SQ SEQUENCE 662 AA; 73780 MW; 2841046199FB1E04 CRC64;
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Query Match 70.9%; Score 2549.5; DB 2; Length 662;  
Best Local Similarity 74.0%; Pred. No. 5.2e-122;  
Matches 512; Conservative 53; Mismatches 90; Indels 37; Gaps 15;

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QY 1 MSDSNQNNQNTQOYSONGNQOQGNRYQGY-QAYNAQAQAGGYYQNTQYSGYQOQG 59
DB 1 MSDPNQ-NGQ-----QGGQAGGNYQOYFQKLTQQAQ-AGGGYQPYGGYGY--GG 49
QY 60 YOYNFDPAGYQOQYNPQGGYQ-QYNPQGGYQOQFNPQGGRGNYKNFNNNNLQYQAGFQ 118
DB 50 YGGYQPYGGYQOQFY--QDGOQAQGAINGYQPYQ--AQGAPGGFN--NYYNQFQP-----Q 98
QY 119 PQSQGHSINDFQKQ---KQAAKPKKTKLVSSSGIKLANATKKVCTKPAESDKKEEK 175
DB 99 QSQGSMTLDDFHQKQTSQAPFKQKSLKLVSSSGIKLANATK---KPKEDKKEEEP 154
QY 176 SATK--EPTKPTKVEEPVKKEKPVOTEKTEESKELPKVDLKLSESTHNTNNANVT 233
DB 155 KKEEKAAPKEQSKKEEP-KRGTTPPAAAKDEKEDLPLEKLKIKE---EQAAANAS 210
QY 234 SADALIKEQEEEDVVDNMFQGDHVSILFMGHVDAGKSTMGGNLLYLTGSDVKRTIE 293
DB 211 GADSLIKEQEEEDVVDNMFQGDHMSIIFMGHVDAGKSTMGGNLLYMTGSDVKRTVE 270
QY 294 KYREAKDAGROGWYLSWMDTNKEBRNDGKTIIEVGKAYFETEKRRYTLIDAPGHKMYVS 353
DB 271 KYREAKDAGROGWYLSWMDTNREERDDGKTIIEVGRAYFETEKRRYTLIDAPGHKMYVS 330
QY 354 EMIGGASQADVGVLVTSARKGEYETGFERGGQTRHALLAKTOGVNKMVVVNMDDPTV 413
DB 331 EMIGGASQADVGVLVTSARKGEYETGFERGGQTRHALLAKTOGVNKLIVTNKDDPTV 390
QY 414 NWSKERYDQCVSNVSNFLRAIGNIKTDVVFMVPSYSGANLKHVDPKCEPNVGTPTLL 473
DB 391 NWSKERYDQCVKLSNPLKAIGNVKEEVVFMVPSYSGAGLGTTRVDPKCEPNVGTPTLL 450
QY 474 EYLDTMNVHVRHINAPFPLPIAAKMDLGTIVGKTESGHIKQOSTLLMPNKTAVEIQN 533
DB 451 EYMDNMSHVDKRNAPFPLPIAAKMDMGTVFSGKIESGHIRKGHSTLLMPNKIPVEIQN 510
QY 534 IYNETENEVDMAKMGQVQLRIKGVBEEDISPGFVLTSKPNPKSVTKFVAQIAVELKS 593
DB 511 IYNETENEVDMAKMGQVQLRIKGVBEEDISPGFVLTSKPNPKSVTRFVAQIAVELKS 570
QY 594 IIAAGFSCVMHVHTAIEEVHIVKLLHLEKGTNRKSKPPAFKMGKVIATLEAPVC 653
DB 571 ILSSGFSCVMHVHTAIEEVHITKLLHLKLRGTNRKSKPPAFKMGKVIATLEAPVC 630
QY 654 VETQYDYPQLGRFLTRDQGTIIAGIKVIAE 685
DB 631 VETQYDYPQLGRFLTRDQGTIIAGIKVIAE 662

RESULT 8
Q6CQF8 PRELIMINARY; PRT; 700 AA.
ID Q6CQF8
AC Q6CQF8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similarity.
GN ORFNames=KLLA0D17424g;
OS Kluyveromyces lactis NRRL Y-1140.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=284590;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NRRL Y-1140;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
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Qy 55 YQ-QGGYQQYNP-DAGYQQQYNPQGGYQQ-QYNPQGGYQQQFNPQGGRGNYKNFNNNNLQ 111
Db 54 QQQYGGNQNQYQGGYQQNNRGGYQQGYNRGGYQQNNY---NRGGYQGNQNNQY 110
Qy 112 GYQA-GFQP-----SQSGSLNDFQKQ--QKQAA---PKPKTKTLKLVSSSGIKLANATK 159
Db 111 GYQYNSQPQQQQQQSQSGSLADFQKQTEQQQAHLNKPVKTKTLKLAGSSGIKLANATK 170
Qy 160 KVGT--KP-----AESDKBEKSAETKEP-----TKEPTKVEEPVK 194
Db 171 KVDTTSPQSKESSPAPAPASASASAPQEBKEKEKEAAAAAPAAPETKTSAPAEK 230
Qy 195 KEKPVTEETKEKSELKVEDLKISESTHTNNANVTADALIKQEVEEDVDVNDM 254
Db 231 KEATP--TPAANKESTIPAAAANK--ESTPVSNSASVATADALUKEQDEIDEVEVDKM 286
Qy 255 FGGKHVSLIFMGHVDAGKSTMGNNLLYLTGSDVKRTIEKYEREAKDAGRQGWLSWMD 314
Db 287 FGGKHVSLIFMGHVDAGKSTMGNNLLYLTGSDVKRTIEKYEREAKDAGRQGWLSWMD 346
Qy 315 TNKEERNDGKTIEVGKAYFETEKRRYTLDPAGHKMTVSEMIIGGASQADVGLVISARKG 374
Db 347 TNKEERNDGKTIEVGKAYFETDKERYTLDPAGHKMTVSEMIIGGASQADVGLVISARKG 406
Qy 375 EYETGFERGGOTREHALLAKTQGVNKMVVVNNKMDPTVNNWKERYDQCVSNYSNFLRAI 434
Db 407 EYETGFERGGOTREHALLAKTQGVNKKIIVVNNKMDSTVGMSKERYQECITKLGAFUKGI 466
Qy 435 GYNLKTDFVMPVPSVSGYSGANLKHVDPKCEPWYTGPTLLLEYLDTMNVHVDHRINAPFMPLI 494
Db 467 GY-AKDDIIYNPVSQYTGAGLKDQVDPKCPWYDGPSSLEVLNDMTWNRKINGPFWMPV 525
Qy 495 AAKMKDGLTIVEGKIESGHIKKGOSTLMPNKTAVEIQNIYNETENEVDAMCQGVKLR 554
Db 526 SGKMKDLGTIVEGKIESGHVKKGNLIMPNKPTPIEVLTFNETEQBCDTAFSGEQVRLK 585
Qy 555 IKGVEEDISPGFVLTPSPKPIKSVTKFVAQIAIVELKLSIIAAGFSCVMHVHTAIEVHI 614
Db 586 IKGIEEDLPQGYVLTSPKPNPKVTTRPEAQIAIVELKLSILNSGFCVMHLHTAIEVKF 645
Qy 615 VKLHLKEKGTNRKSKPPPAFAKGMKVIAVLETPAVCVETDYDYPQLGRFTLRDQGT 674
Db 646 IELGHLEKGTNRKSKPPPAFAKGMKIIAILEVGELVCAETKYDYPQLGRFTLRDQGT 705
Qy 675 IAICKIVKI 683
Db 706 IAIGKITKL 714
```

## RESULT 13

```
Q6Q7I3 PRELIMINARY; PRT; 435 AA.
ID Q6Q7I3;
AC Q6Q7I3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Translation termination factor SUP35 (Fragment).
GN Name=SUP35;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M22, S288C, and M8;
RX PubMed=15059259;
RA Fay J.C., McCullough H.L., Sniegowski P.D., Eisen M.B.;
RT "Population genetic variation in gene expression is associated with
RL phenotypic variation in Saccharomycetes cerevisiae.";
DR EMBL; AY553987; AAS64328.1; -.
DR EMBL; AY553990; AAS64331.1; -.

```

```
DR EMBL; AY553985; AAS64326.1; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003747; F:translation release factor activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0006415; P:translation termination; IEA.
DR InterPro; IPR000795; ProtSyn GTPbind.
DR InterPro; IPR003285; Yeast ERF.
DR PRINTS; PR00315; ELONGATNFCT.
DR PRINTS; PR01343; YEASTERF.
DR PROSITE; PS00301; EFATOR_GTP; UNKNOWN_1.
KW GTP-binding; Protein biosynthesis.
FT NON TER 1 1
FT NON TER 435 435
SQ SEQUENCE 435 AA; 48968 MW; ED0E85699BB28442 CRC64;

Query Match 64.1%; Score 2303; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.1e-109;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NNQNTQOQYSONGNNQOQGNRRYQGYQAYNAQAOPAGGYQNYQYSGYQQGGYQQYNPDA 67
Db 1 NNQNTQOQYSONGNNQOQGNRRYQGYQAYNAQAOPAGGYQNYQYSGYQQGGYQQYNPDA 60
Qy 68 GYQQQYNPQGGYQQYNPQGGYQQQFNPQGGRGNYKNFNNNNLQGYQAGFQPSQGMSLN 127
Db 61 GYQQQYNPQGGYQQYNPQGGYQQQFNPQGGRGNYKNFNNNNLQGYQAGFQPSQGMSLN 120
Qy 128 DFQKQQAAPKPKTKTLKLVSSSGIKLANATKKVGTKPAESDKKEEKSATKEPTKEPT 187
Db 121 DFQKQQAAPKPKTKTLKLVSSSGIKLANATKKVGTKPAESDKKEEKSATKEPTKEPT 180
Qy 188 KVEEPVKKEKPVQTEKTEKSELKVEDLKISESTHTNNANVTADALIKQEVEED 247
Db 181 KVEEPVKKEKPVQTEKTEKSELKVEDLKISESTHTNNANVTADALIKQEVEED 240
Qy 248 DEVVNDMFGGKHVSLIFMGHVDAGKSTMGNNLLYLTGSDVKRTIEKYEREAKDAGRQGW 307
Db 241 DEVVNDMFGGKHVSLIFMGHVDAGKSTMGNNLLYLTGSDVKRTIEKYEREAKDAGRQGW 300
Qy 308 YLSWMDTNKEERNDGKTIEVGKAYFETEKRRYTLDPAGHKMTVSEMIIGGASQADVGL 367
Db 301 YLSWMDTNKEERNDGKTIEVGKAYFETEKRRYTLDPAGHKMTVSEMIIGGASQADVGL 360
Qy 368 VISARKGEYETGFERGGOTREHALLAKTQGVNKMVVVNNKMDPTVNNWKERYDQCVSNV 427
Db 361 VISARKGEYETGFERGGOTREHALLAKTQGVNKMVVVNNKMDPTVNNWKERYDQCVSNV 420
Qy 428 SNFLRAIGYNIKTDV 442
Db 421 SNFLRAIGYNIKTDV 435
```

## RESULT 14

```
Q6Q7I6 PRELIMINARY; PRT; 435 AA.
ID Q6Q7I6;
AC Q6Q7I6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Translation termination factor SUP35 (Fragment).
GN Name=SUP35;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M5;
RX PubMed=15059259;
RA Fay J.C., McCullough H.L., Sniegowski P.D., Eisen M.B.;
RT "Population genetic variation in gene expression is associated with
RL phenotypic variation in Saccharomycetes cerevisiae.";
DR EMBL; AY553987; AAS64328.1; -.
DR EMBL; AY553990; AAS64331.1; -.

```



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 1, 2005, 18:05:05 ; Search time 191.103 Seconds

(without alignments)  
1386.327 Million cell updates/sec

Title: US-09-591-632-2

Perfect score: 3594

Sequence: 1 MSDSNQGNQYQYQSQNG.....FTLRDQGTIIAGIKIVKIAE 685

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: geneseqp1980s:.\*  
2: geneseqp1990s:.\*  
3: geneseqp2000s:.\*  
4: geneseqp2001s:.\*  
5: geneseqp2002s:.\*  
6: geneseqp2003as:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3594	100.0	685	AAB30792	Aab30792 Amino aci
2	3594	100.0	685	ABR53107	Abf53107 Protein s
3	3594	100.0	685	ADK63022	Adk63022 Disease t
4	2347.5	65.3	721	ABP73437	Abp73437 Candida a
5	2345.5	65.3	715	AAB30820	Aab30820 Amino aci
6	2177	60.6	741	AAB30819	Aab30819 Amino aci
7	1679.5	46.7	690	ADS44300	AdS44300 Bacterial
8	1658	46.1	720	ADB70240	Abf70240 C. neofo
9	1557.5	42.3	716	ABJ26050	Abj26050 Aspergill
10	1519.5	43.3	712	ABJ25450	Abj25450 Aspergill
11	1364.5	38.0	634	ADM04489	Adm04489 Human pro
12	1354.5	37.7	499	ADC35080	Adc35080 Human bre
13	1354.5	37.7	499	ADN03793	Adn03793 Antipsori
14	1354.5	37.7	499	ADP54304	Adp54304 Human PRO
15	1354.5	37.7	499	ADP24765	Adp24765 PRO poly
16	1354.5	37.7	499	ADR99225	Adr99225 G1 to S p
17	1346.5	37.5	628	ADN99777	Adn99777 Novel hum
18	1345.5	37.4	628	ADN92825	Adn92825 Human pro
19	1329	37.0	271	AAB30800	Aab30800 A modifie
20	1316.5	36.6	619	ABB62309	Abb62309 Drosophi
21	1307.5	36.4	499	AAW37508	Aaw37508 Human GSP
22	1307.5	36.4	499	ABR56523	Abf56523 Human GSP
23	1307.5	36.4	499	AQD76519	Aqd76519 Amino aci
24	1260	35.1	504	ABR94470	Abf94470 Human pro
25	1097	30.5	215	AAB30799	Aab30799 A modifie

26	922.5	25.7	684	4	AAB68535	Aab68535 Human GNP
27	920.5	25.6	684	4	ABR95757	Abf95757 Human pro
28	825	23.0	661	4	ABR58653	Abf58653 Drosophi
29	824	22.9	449	7	ADD90630	Abd90630 Porphyra
30	823.5	22.9	408	5	ABR90306	Abf90306 Human pol
31	823	22.9	460	8	ADS44204	AdS44204 Bacterial
32	822	22.9	460	8	ADN19715	Adn19715 Bacterial
33	817.5	22.7	408	2	AY27924	Aay27924 Human sec
34	817.5	22.7	408	6	ABO14428	Abf14428 Novel hum
35	817.5	22.7	408	8	ADG78836	Adg78836 Human sec
36	817.5	22.7	408	8	ADN61126	Adn61126 Human sec
37	808	22.5	449	7	ADC81653	Adc81653 Leishmani
38	801.5	22.3	447	2	AAR31594	Aar31594 61-1 clon
39	801.5	22.3	462	2	AAW11237	Aaw11237 Elongatio
40	799.5	22.2	460	2	AAW36114	Aaw36114 Yeast elo
41	798.5	22.2	448	2	AAR05565	Aar05565 Plant elo
42	798.5	22.2	448	2	AAR31595	Aar31595 LeEF-1 cl
43	798.5	22.2	449	3	AAG45359	Aag45359 Arabidops
44	798.5	22.2	449	3	AAJ47144	Aaj47144 Arabidops
45	798.5	22.2	449	3	AAJ35730	Aaj35730 Arabidops

#### ALIGNMENTS

RESULT 1  
AAB30792  
ID AAB30792 standard; protein; 685 AA.  
XX  
AC AAB30792;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Amino acid sequence of a yeast Sup35 protein.  
XX  
KW Sup35; phenotype: SCHAG; self-coalesce; higher-order aggregate;  
KW amyloidogenic domain; aggregation; fibril; phenotypic alteration;  
KW gene therapy; disease resistance; plant pigmentation; prion disease.  
XX  
OS Saccharomyces cerevisiae.  
XX  
FN WO200075324-A2.  
XX  
PD 14-DEC-2000.  
XX  
PF 09-JUN-2000; 2000WO-US015876.  
XX  
PR 09-JUN-1999; 99US-0138833P.  
XX  
PA (ARCH-) ARCH DEV CORP.  
XX  
PI Lindquist S, Li L, Ma J, Liu J, Sondheimer N, Scheibel T;  
XX  
DR WPI; 2001-061723/07.  
XX  
DR N-PSDB; AAC86679.  
XX  
PT New nucleic acid encoding chimeric proteins with self-assembly  
PT properties, useful e.g. for diagnosis and treatment of prion diseases,  
PT also related aggregates, fibrils and polymers.  
XX  
PS Claim 11; Page 125-127; 188pp; English.  
XX  
CC The present sequence represents a yeast Sup35 protein. The protein  
CC possesses the prion-like capacity to undergo a self-perpetuating  
CC conformational alteration that changes the functional state of Sup35 in a  
CC manner that creates a heritable change in phenotype. It is used to  
CC construct chimeric polypeptides of the invention, which comprise at least  
CC one SCHAG (self-coalesce into higher-order aggregates) amino acid  
CC sequence fused in frame with a polypeptide of interest (which is other  
CC than a marker protein, a glutathione-S-transferase or a staphylococcal  
CC nuclear protein). The specification also describes chimeric polypeptides  
CC that comprises an amyloidogenic domain that causes aggregation into  
CC fibrils. The chimeric polypeptides are used to prepare polymers with

CC multiple reactivities, e.g. derivatised with enzymes, or specific binding  
CC partners, and useful e.g. for performing multi-step chemical reactions.  
CC They can be used create an inducible, or stable phenotypic alteration in  
CC a cell, e.g. for gene therapy, protein production, imparting disease  
CC resistance to plants, altering plant pigmentation and for diagnosis and  
CC treatment of prion diseases  
XX  
SQ Sequence 685 AA;

Query Match 100.0%; Score 3594; DB 4; Length 685;  
Best Local Similarity 100.0%; Pred. No. 2.9e-241;  
Matches 685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSDSNQGNNOQNYQOYSONGNOQGNRYQGYQAYNAQAOPAGGYQNYQYSGYQGGY 60  
Db 1 MSDSNQGNNOQNYQOYSONGNOQGNRYQGYQAYNAQAOPAGGYQNYQYSGYQGGY 60  
Qy 61 QQYNPDAGYQQOYNPQGGYQQOYNPQGGYQQOYNPQGGYQNYNNNLQGYQAGFPQ 120  
Db 61 QQYNPDAGYQQOYNPQGGYQQOYNPQGGYQQOYNPQGGYQNYNNNLQGYQAGFPQ 120  
Qy 121 SQGMSLNDFOQKQQAAPKPKTKLVSSSGIKLANATKKVGTGTPAESDKKEEKSAETK 180  
Db 121 SQGMSLNDFOQKQQAAPKPKTKLVSSSGIKLANATKKVGTGTPAESDKKEEKSAETK 180  
Qy 181 EPTKEPTKVEEPVKKEEPVQTEKTEKSELPKVEDLKISESTHNTNNANVTSDALIK 240  
Db 181 EPTKEPTKVEEPVKKEEPVQTEKTEKSELPKVEDLKISESTHNTNNANVTSDALIK 240  
Qy 241 EQEEVDVDDVNDMFGKDHVSLIFMGHVDAGKSTMGNNLLYLTGSDKRTIEKEREAK 300  
Db 241 EQEEVDVDDVNDMFGKDHVSLIFMGHVDAGKSTMGNNLLYLTGSDKRTIEKEREAK 300  
Qy 301 DAGRQGWYLSWMDTNKEERNDGKTIIEVGKAYFETEKRRYTILDPAGHKMVMSEMGAS 360  
Db 301 DAGRQGWYLSWMDTNKEERNDGKTIIEVGKAYFETEKRRYTILDPAGHKMVMSEMGAS 360  
Qy 361 QADVGVLVISARKGEYETGFERGGQTRHALLAKTQGVNKMVVMVNMDDPTVNSKERY 420  
Db 361 QADVGVLVISARKGEYETGFERGGQTRHALLAKTQGVNKMVVMVNMDDPTVNSKERY 420  
Qy 421 DQCVSNSVNFIRAIGYNIKTDDVFMVPVSGYSGANLKDHPKCEPWTGPTLLEYLPTM 480  
Db 421 DQCVSNSVNFIRAIGYNIKTDDVFMVPVSGYSGANLKDHPKCEPWTGPTLLEYLPTM 480  
Qy 481 HVDRHINAPFMLPTAAKWKDLGTTIVEGKIESGHIKQOSTLLMPNKTAVEIQNIYNEN 540  
Db 481 HVDRHINAPFMLPTAAKWKDLGTTIVEGKIESGHIKQOSTLLMPNKTAVEIQNIYNEN 540  
Qy 541 EVDMAWGEOVKLRKIGVEBEDISPGFVLTS PKNPKSVTKFVAQIAIIVELKSTIAAGFS 600  
Db 541 EVDMAWGEOVKLRKIGVEBEDISPGFVLTS PKNPKSVTKFVAQIAIIVELKSTIAAGFS 600  
Qy 601 CVMHVHTAIEBVHIVKLLHLEKGTNRKSKPPAFKGMKVIAVLETPAPCVETVQDY 660  
Db 601 CVMHVHTAIEBVHIVKLLHLEKGTNRKSKPPAFKGMKVIAVLETPAPCVETVQDY 660  
Qy 661 POLGRFTLRDQGTIIAIGKIVKIAE 685  
Db 661 POLGRFTLRDQGTIIAIGKIVKIAE 685

## RESULT 2

ABR53107

ID ABR53107 standard; protein; 685 AA.

XX AC ABR53107;

XX DT 20-JUN-2003 (first entry)

XX DE Protein sequence #SEQ ID 1079.

XX KW Multiprotein complex; eukaryote; drug target; diagnosis.

XX Saccharomyces cerevisiae.

XX EPI258494-A1.

XX 20-NOV-2002.

XX 20-DEC-2001; 2001EP-00130253.

XX 15-MAY-2001; 2001EP-00111774.

XX (CELL-) CELLZOME AG.

XX Bauer A, Grandi P, Krause R, Kruse UD, Kuester BD;  
XX Marzioch M, Schultz JD, Superti-Furga GD;

XX WPI; 2003-250078/25.

XX N-PSDB; ACC61149.

XX New isolated protein complexes useful for diagnosing a disease or  
XX disorder, or as a target for an active agent of a pharmaceutical,  
XX preferably a drug target in the treatment or prevention of disease or  
XX disorder.

XX Disclosure; SEQ ID NO 1079; 17pp + Sequence Listing; English.

XX The invention relates to multiprotein complexes from eukaryotes. Proteins  
XX of the invention and DNA sequences encoding them are given in records  
XX ABR53107 and ACC61149 respectively. The complexes are  
XX obtainable by using a protein as a bait and isolating the set of proteins  
XX which is attached thereto from cells. Such protein complexes may comprise  
XX up to 30 distinct proteins. Protein complexes of the invention are useful  
XX for diagnosing a disease or disorder, or as a target for an active agent  
XX of a pharmaceutical, preferably a drug target in the treatment or  
XX prevention of a disease or disorder. Note: The sequence data for this  
XX patent is not represented in the printed specification, but is based on  
XX sequence information supplied by the European Patent Office. The complete  
XX document is available on CD-ROM

SQ Sequence 685 AA;

Query Match 100.0%; Score 3594; DB 6; Length 685;  
Best Local Similarity 100.0%; Pred. No. 2.9e-241;  
Matches 685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSDSNQGNNOQNYQOYSONGNOQGNRYQGYQAYNAQAOPAGGYQNYQYSGYQGGY 60

Db 1 MSDSNQGNNOQNYQOYSONGNOQGNRYQGYQAYNAQAOPAGGYQNYQYSGYQGGY 60

Qy 61 QQYNPDAGYQQOYNPQGGYQQOYNPQGGYQQOYNPQGGYQNYNNNLQGYQAGFPQ 120

Db 61 QQYNPDAGYQQOYNPQGGYQQOYNPQGGYQQOYNPQGGYQNYNNNLQGYQAGFPQ 120

Qy 121 SQGMSLNDFOQKQQAAPKPKTKLVSSSGIKLANATKKVGTGTPAESDKKEEKSAETK 180

Db 121 SQGMSLNDFOQKQQAAPKPKTKLVSSSGIKLANATKKVGTGTPAESDKKEEKSAETK 180

Qy 181 EPTKEPTKVEEPVKKEEPVQTEKTEKSELPKVEDLKISESTHNTNNANVTSDALIK 240

Db 181 EPTKEPTKVEEPVKKEEPVQTEKTEKSELPKVEDLKISESTHNTNNANVTSDALIK 240

Qy 241 EQEEVDVDDVNDMFGKDHVSLIFMGHVDAGKSTMGNNLLYLTGSDKRTIEKEREAK 300

Db 241 EQEEVDVDDVNDMFGKDHVSLIFMGHVDAGKSTMGNNLLYLTGSDKRTIEKEREAK 300

Qy 301 DAGRQGWYLSWMDTNKEERNDGKTIIEVGKAYFETEKRRYTILDPAGHKMVMSEMGAS 360

Db 301 DAGRQGWYLSWMDTNKEERNDGKTIIEVGKAYFETEKRRYTILDPAGHKMVMSEMGAS 360

Qy 361 QADVGVLVISARKGEYETGFERGGQTRHALLAKTQGVNKMVVMVNMDDPTVNSKERY 420

Db 361 QADVGVLVISARKGEYETGFERGGQTRHALLAKTQGVNKMVVMVNMDDPTVNSKERY 420









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1,4
Db 212 ESKTEPAKEBEIKNOEPAEAKENVEESKVEAPTAAPVSESEPPAST-PKTEAKASKEV 270
Qy 213 PKVEDLKISESTHNTNANTSDALIKEOEVEEDVNDMFGKDHSIIFMGHVDAG 272
Db 271 AAAAAALKVESQAKESVNTNADALKEOEQEDASIVNDMFGKDHSIIFMGHVDAG 330
Qy 273 KSTMGGNLLYLTSVDRRTIEKEREAKDAGROGWYLSWMDTNKEERNDGKTIEVGKAY 332
Db 331 KSTMGGNLLFLTGAVDKRTVEKEREAKDAGROGWYLSWMDTNKEERNDGKTIEVGKSY 390
Qy 333 FETEKRYTILDAPGHKMYSEMIGGASQADVGVLVLSARKGEYETGFERGGOTREHALL 392
Db 391 FETDKRYTILDAPGHKLYISEMIGGASQADVGVLVLSRKRGEYACFERGGQSREHAIL 450
Qy 393 AKTQGVNKMVVNKMDDPTVNSKERYDQCVSNVSNFLRAIGVNIKTIVVMPVSGYSG 452
Db 451 AKTQGVNKLVVNKMDDPTVNSKERYEBCTTKLAMYLGKVGQY-KGDVLFMPVSGYT 509
Qy 453 ANLKDHDVDPKCPWYTGPTLLLEYLDTNNVDRHINAPFMLPIAAKMKDLGTIVEGKIESG 512
Db 510 AGLKERVSKDAPWYNGPSLLEYLDSMPLAVRKINDPMLPISCKMKDLGTIVEGKIESG 569
Qy 513 HIKGQSTLMPNKTAIVEIQNIYNETENEVDMAKCGQVKLRKIGVBEEDISPGFVLTS 572
Db 570 HVKKGQNLVMPNKTQEVTTIYNETEAEADSAFCGQVRLRLRGIEBEDLSAGYVLSSI 629
Qy 573 KNPISVTKFVAQTAIVELKSIINAGFSCVWHVHTAIEEVHIVKLLHLEKGTNRKSKP 632
Db 630 NHPVKVTRFEQAIAIVELKSIILSTGFCVWHVHTAIEEVTFQLLHNLQKGTNRKSKA 689
Qy 633 PAFKGMKMTAVLETEAPVCVETYQDYPOLGRTFLRDQGTITTAIGKIVKI 683
Db 690 PAFKGMKMTAVLETEPCVIESYDDYPQLGRTFLRDQGTITTAIGKIVTKL 740

RESULT 7
ADS44300
ID ADS44300 standard; protein; 690 AA.
XX ADS44300;
XX
XX 02-DEC-2004 (first entry)
XX Bacterial polypeptide #22730.
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX Bacteria.
XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX

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```

PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 22730; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 690 AA;
SQ

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```

Query Match 46.7%; Score 1679.5; DB 8; Length 690;
Best Local Similarity 51.4%; Pred. No. 4.5e-108;
Matches 332; Conservative 109; Mismatches 148; Indels 57; Gaps 15;
Qy 68 GYQQQVNPQGG--YQQYNPQGGYQQQFNPGQGRGNYNFNNNNLCYQAGFQPSQSGMS 125
Db 74 GFVPVNNIAGGYPYQYTGQ-----QNSNSPHPTKSYQYQYQ-KPTGNT 117
Qy 126 LN-----DFKQKQQAAPKPK-----KTLKL-----VSSSGIKLANATKK 160
Db 118 VDEKSRVPDFSKKSFVPKPAIPKGVLSLGNTPSKSTKPKISISLGGTKAPTTPK 177
Qy 161 VGTKPAESDKKESEKSAETKEPTKEPTKVEEPKKEKPVQTEKTEKSELPKVEDLKI 220
Db 178 AA--PAAQSKTETPAPKVTSESTKETAAPPP---QETP--TKSADAEAKRTSPAPAAAL 230
Qy 221 SESTHNTNNANVTSADALIKEOEVEEDVNDMFGGDHVSILIFMGHVDAGKSTMGNL 280
Db 231 KKAEEAAEPATVTE-DA--TDLQNEVDQELLKDMY-GKEHVNVIFIGHVDAGKSTLGGNI 286
Qy 281 LYLTGSDVKRTIEKYEREAKDAGROGWYLSWMDTNKEERNDGKTIEVGKAYFETEKRY 340
Db 287 LFLTGMDVKRTMEKIEREAKGKESWYLSWALDSTSEEREKGTVEVGRAYFETEHRR 346
Qy 341 TILDAPGHKMYSEMIGGASQADVGVLVLSARKGEYETGFERGGOTREHALLAKTGVNK 400
Db 347 SLLDAPGHKGYVTNNMGASQADIGVLVLSARGEFEAGFERGGOTREHALLAKTQGINH 406
Qy 401 MVTVMNKMDDPTVNSKERYDQCVSNVSNFLRAI-GYNIKTIVVMPVSGYSGANLKDHY 459
Db 407 LVVVINKMDEPVSQWSEERYKECVKLSMFLRRVAGYNSKTDVKYMPVSAITGQNVKDRV 466
Qy 460 DPKECPWYTGPTLLLEYLDTNNVDRHINAPFMLPIAAKMKDLGTIVEGKIESGHIKQGS 519
Db 467 DSSVCPWYQGPSLLEYLDSMTHLERKVNAPFIMPIASKYKDLGTILEGKIEAGSIKKNS 526
Qy 520 TLLMPNKTAIVEIQNIYNETENEVDMAKCGQVKLRKIGVBEEDISPGFVLTSPPNPKSV 579
Db 527 VLVMPIQTLEVTIAIYDEADEEIESSISICGQDVRLVRG-DSDSVQTYGVLTTSTKNPVHAT 585

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Qy	580	TKFVAQIAIVELKSIAGFSCVMHVHTAIBEVHIVKLLHLKLEKGTNRKSKPPAPAKG	634
Db	586	TRFIAQIAILELPSLITTGYSWVHIHTAVEVSFAKLHLKLDK-TNRKSKPPMEATKG	644
Qy	640	MKVIIVLETEAPVCVETVODYPQLGRFTLRDQGTIIAGIKIVKIAE	685
Db	645	MKIIAELETQTPVCMERFEDYQYMGRTLRDQGTIVAGKVVKILD	690
<p>             RESULT 8              ADB70240              ID ADB70240 standard; protein; 720 AA.              XX ADB70240;              XX              XX 04-DEC-2003 (first entry)              DT              XX C. neoformans amino acid sequence SEQ ID NO:3284.              DE              XX fungicide; gene therapy; infection.              KW              XX Cryptococcus neoformans.              XX              XX WQ2003052076-A2.              PN              XX              XX 26-JUN-2003.              PD              XX              XX 17-DEC-2002; 2002WO-US040225.              XX              XX 17-DEC-2001; 2001US-0341261P.              PR              XX (ELIT-) ELITRA PHARM INC.              PA              XX Zamudio C, Eroshkin AM;              XX              XX WPI; 2003-533017/50.              DR              XX N-PSDB; ADB69157.              XX              XX New nucleic acid, useful for preparing a composition for treating an              PT infection caused by Cryptococcus neoformans.              PT              XX Claim 9; SEQ ID NO 3284; 136pp; English.              PS              XX The invention relates to a novel purified or isolated Cryptococcus              XX neoformans nucleic acid molecule comprising a sequence encoding a              CC polypeptide comprising a sequence not given in the specification. A              CC polynucleotide of the invention has fungicide activity, and may have a              CC use in gene therapy. The nucleic acid is useful for preparing a              CC composition for treating an infection caused by Cryptococcus neoformans.              CC The present sequence represents a C. neoformans sequence of the              CC invention. Note: The sequence data for this patent is not represented in              CC the printed specification, but was obtained in electronic format directly              CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.              XX              XX Sequence 720 AA:           </p>			
Qy	38	QAQAGGYQNYQGYSGYQGGYQOQYNPDAGYQOQYNPQGGYQOQYNPQGGYQOQFNPOGG	97
Db	48	QQQPFDPY-----GQQQGGYPQYG-----QYQOQGGYPQYQYGGYPQ-----	86
Qy	98	RGNYNFNWNNNLQGYQA-----GFQPSQSGMSLNDFFQOQQAAPKPKTKLKLV	148
Db	87	-----QGYVPFGAPGAPRAYQP-POARNVQGFQPPFSFSSPAPPDTPKAPA	132
Qy	149	SSGIIKLA---NATKVGVTKEPAESDKKEEKSATKEPTKVEPEPVKKEE---KPQV	201
Db	133	GXPVLSLTGGCGAPK---AAPSLSTIEKASSKSPKPAAPTPKAPAKGEAASAPVS	189
Qy	202	TEEKTEESKSELPKVEDLK-----ISBSTHTNNNNTS-----AD	236
Qy	202	TEEKTEESKSELPKVEDLK-----ISBSTHTNNNNTS-----AD	236

[illegible]

New purified or isolated nucleic acids of essential genes of *Aspergillus fumigatus*, useful for treating or preventing infections by *A. fumigatus*, or for treating a non-infectious disease in a subject e.g. cancer.











Db	476 RFTLRDEGKTIAGIKVLKL 494	
ADP24765		
ID	ADP24765 standard; protein; 499 AA.	
AC	ADP24765;	
XX	18-NOV-2004 (first entry)	
DE	PRO polypeptide SEQ ID NO:1943.	
KW	PRO: antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;	
KW	osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;	
KW	antiaethmatic; hepatotropic; respiratory; gene therapy; immune system.	
OS	Unidentified.	
XX	WO2004041170-A2.	
XX	21-MAY-2004.	
XX	30-OCT-2003; 2003WO-US034312.	
XX	01-NOV-2002; 2002US-0423394P.	
XX	(GETH ) GENENTECH INC.	
XX	Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WT;	
XX	Wu TD;	
XX	WPI; 2004-419628/39.	
XX	N-PSDB; ADP24764.	
XX	New PRO polypeptides and polynucleotides, useful for treating e.g.	
XX	erythematosis, rheumatoid arthritis, diabetes mellitus, immune-mediated	
XX	renal disease, or demyelinating diseases of the central or peripheral	
XX	nervous system.	
XX	Claim 7; SEQ ID NO 1943; 2940pp; English.	
XX	The invention relates to a novel isolated nucleic acid and the PRO	
XX	polypeptide encoded by it. A protein of the invention has	
XX	antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,	
XX	osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,	
XX	antiaethmatic, hepatotropic, and respiratory activity. A polynucleotide	
XX	of the invention may have a use in gene therapy. The PRO polypeptide, its	
XX	agonist, antagonist, or antibody that specifically binds to the	
XX	polypeptide is useful for treating an immune related disorder such as	
XX	systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,	
XX	juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an	
XX	idiopathic inflammatory myopathy, Sjogren's syndrome, autoimmune	
XX	vasculitis, sarcoidosis, autoimmune haemolytic anaemia, systemic	
XX	thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal	
XX	disease, a demyelinating disease of the central or peripheral nervous	
XX	system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,	
XX	a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary	
XX	disease, infectious or autoimmune chronic active hepatitis, primary	
XX	biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,	
XX	inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's	
XX	disease, an autoimmune or immune-mediated skin disease, a bullous skin	
XX	disease, erythema multiforme, contact dermatitis, psoriasis, an allergic	
XX	disease, asthma, allergic rhinitis, atopic dermatitis, food	
XX	hypersensitivity, urticaria, an immunologic disease of the lung,	
XX	eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity	
XX	pneumonitis, a transplantation associated disease, graft rejection or	
XX	graft-versus-host disease. The present sequence represents a PRO protein	
XX	of the invention.	
XX	Sequence 499 AA;	

GenCore version 5.1.6  
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OM protein - protein search; using sw model

Run on: July 1, 2005, 18:06:15 ; Search time 40.0283 Seconds

(without alignments)  
1646.548 Million cell updates/sec

Title: US-09-591-632-2

Perfect score: 3594

Sequence: 1 MDSNQGNQNNYQQYQSQG.....FTLRDQGTTAIGKIVKIAE 695

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:.\*  
1: Pirl.\*  
2: Pirl2.\*  
3: Pirl3.\*  
4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3594	100.0	685	1 EFBYS2	suppressor 2 prote
2	2177	60.6	741	2 S12921	suppressor 2 prote
3	1719	47.8	729	2 T51896	probable translati
4	1689	47.0	662	2 T41442	omnipotent nonsens
5	1675	46.6	662	2 T51948	omnipotent nonsens
6	1375	38.3	614	2 S58444	SUP35 protein - Af
7	1354.5	37.7	499	2 S06941	suppressor 2 prote
8	1283.5	35.7	515	2 T03717	GTP-binding protei
9	1213.5	33.8	573	2 T23102	hypothetical prote
10	1160.5	32.3	409	2 T03718	suppressor 2 prote
11	946.5	26.3	280	2 T43011	suppressor protein
12	859.5	23.9	435	2 A49171	translation elonga
13	847	23.6	441	2 S54734	translation elonga
14	844	23.5	456	2 S11665	translation elonga
15	836.5	23.3	449	2 A54760	translation elonga
16	833	23.2	458	2 S35894	translation elonga
17	831	23.1	458	2 A35154	translation elonga
18	829	23.1	458	2 S06300	translation elonga
19	829	23.1	460	2 S35772	translation elonga
20	828.5	23.1	449	2 JC5117	translation elonga
21	826	23.0	435	2 S43507	translation elonga
22	825.5	23.0	460	2 S43861	translation elonga
23	825	23.0	458	2 A25938	translation elonga
24	823	22.9	460	2 T41617	translation elonga
25	822.5	22.9	457	2 S35986	translation elonga
26	822	22.9	460	2 T38230	translation elonga
27	821	22.8	435	2 H90162	hypothetical prote
28	821	22.8	459	2 JC4253	translation elonga
29	819	22.8	460	2 T42089	translation elonga

30	817	22.7	460	2 T43267	translation elonga
31	814.5	22.7	460	2 JC4214	translation elonga
32	813.5	22.6	460	2 T47258	translation elonga
33	812	22.6	444	2 T44963	translation elonga
34	808.5	22.5	461	2 T43704	translation elonga
35	806.5	22.4	446	2 S16308	translation elonga
36	802	22.3	459	2 S59595	translation elonga
37	800	22.3	460	2 T43894	translation elonga
38	799.5	22.2	449	2 S08534	translation elonga
39	798.5	22.2	448	2 S10507	translation elonga
40	798.5	22.2	449	2 S06724	translation elonga
41	798.5	22.2	967	2 F86214	protein T6D22.2 [i
42	798	22.2	437	2 C72570	probable translati
43	797.5	22.2	458	1 EFBY1A	translation elonga
44	797	22.2	462	2 A60491	translation elonga
45	796.5	22.2	462	1 EPHU1	translation elonga

#### ALIGNMENTS

##### RESULT 1

EFBYS2

suppressor 2 protein - yeast (Saccharomyces cerevisiae)

N;Alternate names: G1-to-S transition protein; protein YD9395.05; protein YDR172W

C;Species: Saccharomyces cerevisiae

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004

C;Accession: S00733; JT0323; S49768; S00488; A26742; S00533; S05723

R;Wilson, P.G.; Culbertson, M.R.

J. Mol. Biol. 199, 559-573, 1988

A;Title: SUP12 suppressor protein of yeast. A fusion protein related to the EF-1 family

A;Reference number: S00733; MUID:88172503; PMID:3280807

A;Accession: S00733

A;Molecule type: DNA

A;Residues: 1-685 <WIL>

A;Cross-references: UNIPROT:P05453; EMBL:X07163; NID:g4581; PIDN:CAA30155.1; PID:g4582

R;Kushnir, V.V.; Ter-Avanesyan, M.D.; Telckov, M.V.; Surguchov, A.P.; Smirnov, V.N.; I

Gene 66, 45-54, 1988

A;Title: Nucleotide sequence of the SUP2(SUP35) gene of Saccharomyces cerevisiae.

A;Reference number: JT0323; MUID:88329727; PMID:3047009

A;Accession: JT0323

A;Molecule type: DNA

A;Residues: 1-685 <KUS>

A;Cross-references: EMBL:M21129; NID:gl72789; PIDN:AAA35133.1; PID:gl72791

R;Murphy, L.; Harris, D.E.

submitted to the EMBL Data Library, November 1994

A;Reference number: S49764

A;Accession: S49768

A;Molecule type: DNA

A;Residues: 1-685 <MUR>

A;Cross-references: EMBL:Z46727; NID:gl289283; PIDN:CAA86677.1; PID:gl289287; GSPDB:GN00

R;Kikuchi, Y.; Shimatake, H.; Kikuchi, A.

EMBO J. 7, 1175-1182, 1988

A;Title: A yeast gene required for the G1-to-S transition encodes a protein containing a

A;Reference number: S00488; MUID:88296422; PMID:2841115

A;Accession: S00488

A;Molecule type: DNA

A;Residues: 1-52, 'C', '54'-685 <KIK>

A;Cross-references: GB:Y00829; EMBL:Y00859; NID:g3711; PIDN:CAA68760.1; PID:g3712

C;Genetics:

A;Gene: SGD: SUP35; SUP12; GST1; SUP2; MIPS: YDR172W

A;Cross-references: SGD: S0002579; MIPS: YDR172W

A;Map position: 4R

C;Superfamily: suppressor 2 protein; translation elongation factor Tu homology

C;Keywords: duplication; GTP binding; nucleotide binding; P-loop; phosphoprotein; tandem

F;1-123/Domain: A <DOM1>

F;42-119/Region: 10-residue repeats

F;124-253/Domain: charged <DOM2>

F;159-222/Region: glutamic acid/lysine-rich

F;254-685/Domain: C <DOM4>

F;261-409/Domain: translation elongation factor Tu homology <ETU>

F;267-274/Region: nucleotide-binding motif A (P-loop)

F;406-409/Region: GTP-binding NKXD motif

F;273/Binding site: GTP (Lys) #status predicted

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Query Match      100.0%; Score 3594; DB 1; Length 685;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]

RESULT 2

S12921  
suppressor 2 protein - yeast (Pichia pinus)  
N;Alternate names: SUP2 protein  
C;Species: Pichia pinus  
C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 09-Jul-2004  
C;Accession: S12921  
C;Kushnir, V.V.; Ter-Avanesyan, M.D.; Didichenko, S.A.; Smirnov, V.N.; Chernoff, Y.O.;  
Yeast 6, 461-472, 1990  
A;Title, divergence and conservation of SUP2(SUP35) gene of yeasts Pichia pinus and Saccharomyces cerevisiae  
A;Reference number: S12921; MUID:91181341; PMID:2080663  
A;Accession: S12921  
A:Molecule type: DNA  
A:Residues: 1-741 <KUS>  
A;Cross-references: UNIPROT:P23637; EMBL:X56910; NID:G3235; PIDN:CAA40231.1; PID:G3236  
C;Genetics:  
A:Gene: SUP2  
C;Superfamily: suppressor 2 protein; translation elongation factor Tu homology

A; Cross-references: EMBL:AL391572; GSPDB:NC00116; NCSP:B23111.80  
A; Experimental source: BAC clone B23111; strain OR74A  
C; Geneticals:  
A; Gene: NCSP:B23111.80  
A; Map position: 6  
A; Introns: 111/1; 711/3  
C; Superfamily: suppressor 2 protein; translation elongation factor

Query Match	47.8%;	Score 1719;	DB 2;	Length 729;
Best Local Similarity	49.9%;	Pred. No. 1.3e-81;		
Matches 365;	Conservative 98;	Mismatches 204;	Indels 64;	Gaps 15;
QY	7	GNNQNYQ-----OYSGNNGOQGNRRYQGYOAYNA-----	37	
DB	3	GNVQNNWEAAADQDERLARQTOQMNINAGTFR-PGAAAFTPGAPSTPGQFAAPGTPQ	61	
QY	38	-QAQPAAGYQNY-QYSGYQGGYQOYNPDAGYQOQYNPQGGYQOYNPQGGYQOYNPQ	95	
DB	62	YQOQYVGAQOQYGGYQOYQGGYQOYQGGYQOYQGGYQOYQGGYQOYQGGYQOYQGGY	119	
QY	96	GGRGNY-KNFYNNNLQYQAGFQPOQSGHSLND---FQKQKQAAPK----	144	
DB	120	QQYGGYQOQYQOQOQNNDAPKAPQPIVKRPEQAAQAPKADAPKATAAPVKVLSVG	179	
QY	145	-----KLVSSSGKILANATKKV---GTPAESDKKEBEKSAETKEPTKVPBPVKKE	196	
DB	180	GDAPAKVLSIGGDAPKPAKVLSISGTAPA---KEEPPKEAAKKEGTAEAAAKVTATKAV	236	
QY	197	EKPVQTEKTEKSELPKVEDLKLISESTHNTNANVTSDALIKE-QEEEVDDVNDMF	255	
DB	237	QK---TESAAASGRTPSPSGRASPAAKSGNKVSRDQDAVEKDIQSADVDEDTLKEIY	293	
QY	256	GKDHVSLIPMGHVDAKSTMGGNLLYLTSQVDKRTIEKYEREAKDAGCGWYLSWMDT	315	
DB	294	-GKEHNNIIFIGHVDAKSLTGGAIFYTGMDORTLDYKREAKOMGRETWYLSWALDL	352	
QY	316	NKBERNDGKTIYEVKAYFETEKRRYTILDAFGRHMYVSEMIGGASQADVGVLVISARKGE	375	
DB	353	TNEERAGKKTVEVGRGPFETDKRYSILDPAGHKTYVPMNIGGASQADVGILVISARKGE	412	
QY	376	YETGFERGGOTREHALLAKTQGNKMWVNVNKMDDPTVNSKERYDCOVSNVNFLEAIG	435	
DB	413	YETGFERGGOTREHALLAKTQGNKLVVNVNKMDDPTVNSSEERYCKEKTLLAQFLKGTG	472	
QY	436	YNIKTDVVPVSVGSGANLKHVDPKCEPWYTGPTLLEYLDTMNVHVRHINAPFMLPIA	495	
DB	473	YNLKTDFVFPVAAQQTWGIKDRVPKDLCPWYDGPSSILEYLDNMSSLERKVNAPFMMAVS	532	
QY	496	AKMKDLGTIVEGKIESGHIKKGSTLLMPNKTAVEIQNIYNETENEYDMAMCGSQVKLRI	555	
DB	533	GKYRDMGTMEGKIEAGVKKGMSLIMPNKQSTIEISAVYGETEDEVPAQCGQOVLRL	592	
QY	556	KGYVEEDISPGFVLTSQKNPIKSVTKQVAQIAIVELKSIITAGSGSCVMVHTALEEVHIV	615	
DB	593	RGIEEIEIMPFGVLCSPKRLVHNVTAPFAQIRILDLSILTAGFNCVLHVHAAIEEYVTF	652	
QY	616	KLHLKELKGTNRKSKPPAPAKGMKVIIVLET---EAPVCVETYQDYPOLGRETLRDOG	672	
DB	653	ALLHLKQGTNRKSKLPPSHAKGDSIARLEVTGGAGSCVFERFEDYPQMGRETLRDOG	712	
QY	673	TTTIAIGKIVKI	683	
DB	713	QTTAIGKITKL	723	

RESULT 4  
T41442  
omnipotent nonsense suppressor, efi alpha factor-like gtp-bindingprotein - fission yeast  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T41442  
R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, October 1998

A;Reference number: Z21993  
A;Accession: T41442  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-662 <SEE>  
A;Cross-references: UNIPROT:O74718; EMBL:AL012824; I  
A;Experimental source: strain 972h; cosmid c584

[illegible]

RESULT 5  
T51948  
omipotent nonsense suppressor SUP35/erf-3 - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004  
C;Accession: T51948



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Best Local Similarity 49.6%; Pred. No. 2.8e-59;
Matches 254; Conservative 89; Mismatches 148; Indels 21; Gaps 7;

Qy      185 EPTKVPEPVKE---EKPVQTBEKTEESKELPKVEDLKISSETH-----NTNNANVTS 234
Db      5 EDGKPSEAIPKPTNGEDSASAWAEGEAGDDEKPDIDPEDELKDRAHPDLEKPNVEPKGIAG 64

Qy      235 ADALIKQEBEVDDEV-VNDMPFGKGKHVSLLFMGHVDVAGKSTWGNLNYLTGSVDKRTIE 293
Db      65 KEA---SPBEDIQDEVEVK---KRLNVVFVIGHVDVAGKSTTGQGLLSGGQVDDRTTIQ 117

Qy      294 KYBREAKDAGRCQGWSYLSSVMWDTNKBENRDKTIEVGKAYPETEKRRYTTILDAPGHKNVYS 353
Db      118 KYBREAKDNKRESWNWAYIMDTNEBERVKGITVEVGRAHFEETDTTFITILDAPGHKSYP 177

Qy      354 EMTCGASQADVGVLVVISARKGEYETGFPERGQGTREHALLAKTOGVNKVVVVNMKMDPTV 413
Db      178 NMISGRSQADIGLLVISARKGEFETGYERGQGTREHVQLAKTLGVTKFLVVVNKMMDPTV 237

Qy      414 NWSKERYDCVCNVSNVNFPLRAIGNYNITDVVPMVPVSGYGANLKHVDHPDKPCPWYTGTPLL 473
Db      238 NWSKERYDETESKNVPFLRSSGGYNVKDVQFLPISGLLGSLNLKTRMEKSVCPWMNGPCLF 297

Qy      474 EYLDTNHVDHRHNAPMLPIAAKMKDLGTIVIEGKTIESGHIKKQSOTLLMKNKTAVEIQN 533
Db      298 ETLDVAVEVPRDPNGPLRMPIIDKFDMGVFVNMCKTESGSIHEGDNLIILIIPNKAADVLA 357

Qy      534 IYNETEENEVDMAWCGEQVKLRIRKGVEEEDISPQFVLTSKPNPTKSVTKFVAQIAVEL-- 591
Db      358 IFCD-EDKVHVHCVPGENVRVLSGVSEDDILSGFVLCVSNAKPIHAVTEFVAQQLILELD 416

Qy      592 KSIIAAGFCSCMHVHTAIBEHVHIVKLHLKLEKGTNRKSKPPAPAKGMKVIAVLETEAP 651
Db      417 NAIFTAGYKAVLIHSWECEIIVELMQOIDLTKTKPMKKKPLFKVNGAIVLCRVQVNNL 476

Qy      652 VCVEYTDQIPOLGRFTLRDOGTIIATGKI VKI 683
Db      477 ICVEKFSDFQAQLGRFTLRTEGKTVAVGKITAL 508

RESULT 9
T23102
hypothetical protein H19N07.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23102
R;Dobson, R. submitted to the EMBL Data Library, March 1997
A;Reference number: Z19678
A;Accession: T23102
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-573 <NIL>
A;Cross-references: UNIPROT:O45622; EMBL:Z92835; PIDN:CA807395.1; GSPDB:GN00023
A;Experimental source: clone H19N07
C;Genetics:
A;Gene: CESP:H19N07.1
A;Map position: 5
A;Introns: 40/1; 80/3; 216/3; 505/3
C;Superfamily: suppressor 2 protein; translation elongation factor Tu homology
F;110-258/Domain: translation elongation factor Tu homology <EU>

Query Match 33.8%; Score 1213.5; DB 2; Length 573;
Best Local Similarity 39.6%; Pred. No. 1.4e-55;
Matches 252; Conservative 115; Mismatches 158; Indels 111; Gaps 12;

Qy      96 GGRGNTKFNFNYNLNLOGYAQGFQSQGMSLNDFOKQKOAAKPKKTLKLVSSEGKILA 155
Db      3 GWNVNASFFVPVNPANRPFPVG-QP-----YTPQPEQAAPTEPTWEDAQAD----- 46

Qy      156 NATKKVGTGTPAESDKKEEBSKA-----ETKPTKPTKVPVEPKKEEKPVQTEETEEK 209
Db      47 --TSPAADOPEVAEPVAVOESAPVAVPSATPAEPKGPTEEDLVLPALKAFQ----- 96

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Qy 210 SELPKVEDLKISESTHNTNNAVTSADALIKEQEEVEVDDEVNDMFGGKHVSILFMGHV 269
Db 97 -----RTVYVDDGTH-----KEHINMVFVGHV 118
Qy 270 DAGKSTMGNNLLYLTSVDKRTIEKYREAKDAGROGWYLSVWMDTKNEERNDGKTIIEVG 329
Db 119 DAGKSTIGQLMFLTGMVDKRTLEKYREAKEKRESWYLSWMDTNDEREKSKTVEVG 178
Qy 330 KAYPETEKRRYTLIDAPCHKMYSEMIGGASQADVGLVVISARKGEYTFETGPERGGQTRH 389
Db 179 RAYPETEKRRHPTILIDAPGHKSFPVNMIVGANQADLAVLVISARGBEFTGPDGQGQTRH 238
Qy 390 ALLAKTOGVNKMVVVNMKDDPTVNSKERYDQCVSNSVFLRAIGYNIKTDDVVVMPVSG 449
Db 239 SMLVKTAGVHLVILVNMKDDPTVWKEERPEKEGKLITPLRLKLGFNPKTIDTIVPCSG 298
Qy 450 YSGANLADHDVDPKCEPWYTGPTLLEYLDT-MNHVDRHINAPFMLPIAAKMKDLGTIVEGK 508
Db 299 LTGAFIKDRPTGSEGNWYSGCFIEFDVLLPSYKRDENGVRCTVAEKYSEMGTVIIGK 358
Qy 509 IESGHIKKGOSTLMPNKTAVEIQNIYNETENEVDMAWCGEQVKLRIRKGVBEEDISPGFV 568
Db 359 MESGCVQKGDTLVWPNKQPQVQLIWAQ-DVETERVVAGDNIFKFLKGIEENELQGGFI 417
Qy 569 LTSKPNPKSVTKVAQIAVELKSIIAAGFSCVMHVHTAIEEVHI-VKLLHLEKQ--- 624
Db 418 ICSPDSLAKTRGRVDAEVLVLEHRSIIASGVSCLVHIQSAAVEEVTVKVLRLPEELGGCP 477
Qy 625 ----TN-----RKSS--KKPPAFAKGKMKVIAVLETE 649
Db 478 IGGTINSGDWPRPQNGLOAHFNCRTGVTIATIDKTKGKRAKFKVQDEKCIWRLPES 537
Qy 650 APVCVETQYDYPQLGRFLTRDQGTIIAGIKVIAE 685
Db 538 EPFVLEPFKEYPYLGRLFLTRDEGKTIAIGKVLKVE 573

RESULT 10
T03718
suppressor 2 protein homolog - common tobacco (fragment)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03718
R;Brander, K.A.; Owttrim, G.W.; Brunold, C.
Plant Physiol. 108, 1748, 1995
A;Title: Isolation of a cDNA (EMBL X85803) encoding a putative chloroplastic isoform of
A;Reference number: Z15026
A;Accession: T03718
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-409 <BR>
A;Cross-references: UNIPROT:Q40582; EMBL:L38829; NID:g1009233; PIDN:AAA79033.1; PID:g100
A;Experimental source: strain SR1
C;Genetics:
C;Superfamily: suppressor 2 protein; translation elongation factor Tu homology
C;Keywords: GTP binding; nucleotide binding; P-loop
F;386-393/Region: nucleotide-binding motif A (P-loop)

Query Match 32.3%; Score 1160.5; DB 2; Length 409;
Best Local Similarity 55.1%; Pred. No. 4.9e-53;
Matches 220; Conservative 71; Mismatches 105; Indels 3; Gaps 2;

Qy 287 VDKETIKERYEAKDAGROGWYLSWMDTKNEERNDGKTIIEVGKAYFETEKRRYTILDAP 346
Db 5 VDDRTIQKYREAKDKNRESYMAIYMDTNEERVKGITVEGVAHFETDTRFTILDAP 64
Qy 347 GHKMYSEMIGGASQADVGLVVISARKGEYTFETGPERGGQTRHALLAKTOGVNKMVVVN 406
Db 65 GHKSYPNMISGASQADGLVVISARKGEYTFETGPERGGQTRHVLQAKTLGVTKLLVVVN 124
Qy 407 KMDDPTVNSKERYDQCVSNSVFLRAIGYNIKTDDVVMPVSGYSGANLKDHDVDPKCPW 466
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Db 125 KMDDPTVNSKERYDETESKMWPFRLSSGVNVKDVQFLPISGLGSLNLRMEKSCVPW 184
Qy 467 YTGPTLLEYLDTMNVDRHINAPFMLPIAAKMKDLGTIVEGKIESGHIKKGOSTLLMPNK 526
Db 185 WNGPCLFETIDAVEVPPDPNGPLRMPIIDKFDMGTVMVGKIESGSIREGDNLLVMPNK 244
Qy 527 TAVEIQNIYNETENEVDMAWCGEQVKLRIRKGVBEEDISPGFVLTSPKNPPTKSVTKFVAQI 586
Db 245 AAVKLAIFCD-EDKTVHVGFGENVRLSGVEEDDILSGFVLSVAKPHAVTEFVAQL 303
Qy 587 AIVEL--KSIIAAGFSCVMHVHTAIEEVHI-VKLLHLEKGTNRKSKKPPAPAKGKMKVIA 644
Db 304 QILLELDNAIFTAGYKAVLHSHVSECEIVELMQQIDLTKTKPKMKKPLFVKNGAIVLC 363
Qy 645 VLETEAPVCVETQYDYPQLGRFLTRDQGTIIAGIKVIA 683
Db 364 RVQVNNLICVEKFSDFLAQLGRFTLRTEGKTVAVGKITAL 402

RESULT 11
T43011
suppressor protein homolog - fission yeast (Schizosaccharomyces pombe) (fragment)
C;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43011
R;Yoshiohka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A;Reference number: Z17323; MUID:98162722; PMID:9501991
A;Accession: T43011
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-280 <YOS>
A;Cross-references: UNIPROT:P78857; EMBL:D89207; NID:g1749621; PIDN:BAA13868.1; PID:g174
A;Experimental source: strain PR745
C;Superfamily: suppressor 2 protein; translation elongation factor Tu homology

Query Match 26.3%; Score 946.5; DB 2; Length 280;
Best Local Similarity 59.9%; Pred. No. 3.5e-42;
Matches 169; Conservative 56; Mismatches 54; Indels 3; Gaps 3;

Qy 405 VNKMDPTVNSKERYDQCVSNSVFLRAI-GYNIKTDDVVMPVSGYSGANLKDHDVDPKE 463
Db 1 INKMDDESQVSESNKECVDKLSMFLRRVAGYNSKTDVKYMPVSAITGQNVKRDVSSV 60
Qy 464 CPWYTGPTLLEYLDTMNVDRHINAPFMLPIAAKMKDLGTIVEGKIESGHIKKGOSTLLM 523
Db 61 CPWYQGPSLLEYLDSMTHLERKVNAPFIMPDIASKYKDLGTILEGKIEAGSIKKNSNLVM 120
Qy 524 PNKTAVEIQNIYNETENEVDMAWCGEQVKLRIRKGVBEEDISPGFVLTSPKNPIKSVTKFV 583
Db 121 PINQTLSEVTAIYDEADEIESSICGQDQVRLVRG-DDSDVQGTGYVLTSTKNPVAHTTRFI 179
Qy 584 AQIAVELKSIIAAGFSCVMHVHTAIEEVHI-VKLLHLEKGTNRKSKKPPAPAKGKMKVI 643
Db 180 AQIALELPILITGYSVWHIHTAVEEVSFAKLLHLDK-TNRKSKKPPMPFATGKMKII 238
Qy 644 AVLETEAPVCVETQYDYPQLGRFLTRDQGTIIAGIKVIAE 685
Db 239 AELETQTPVCWERFEDYQWGRFTLRDQGTITVAVGKVKVILD 280

RESULT 12
A49171
translation elongation factor eEF-1 alpha chain - Tetrahymena pyriformis
N;Alternate names: 14-nm filament-associated protein
C;Species: Tetrahymena pyriformis
C;Date: 21-Jan-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C;Accession: A49171; B49171
R;Kurasawa, Y.; Numata, O.; Katch, M.; Hirano, H.; Chiba, J.; Watanabe, Y.
Exp. Cell Res. 203, 251-258, 1992
A;Title: Identification of Tetrahymena 14-nm filament-associated protein as elongation f
```



F;156-159/Region: GTP-binding NKXD motif

Query Match 23.5%; Score 844; DB 2; Length 456;  
Best Local Similarity 41.0%; Pred. No. 1.3e-36;  
Matches 176; Conservative 82; Mismatches 161; Indels 10; Gaps 6;  
Qy 258 KDHVSLIFMGHVDAGKSTMGNNLLYLGTSGVDKRTIEKYEREAKDAGRGQWYLSWVMDTK 317  
Db 8 KTHINIVVGHVDAGKSTMGNNLLYLGTSGVDKRTIEKYEREAKDAGRGQWYLSWVMDTK 67  
Qy 318 EERNKGKTIIVGKAYFETEKRRYTIIDAPGHMVMVSEMIGGASQADVGLVISARKGEYE 377  
Db 68 AERERGITIDIALWKFFTSKYFTIIDAPGHRDFIKNMITGTSQADCAVLVIASPTGEFE 127  
Qy 378 TGPERGQOTREHALLAKTQGVNKMVNVKMDPTVNMWKERYDOCVSNVSNFLRAIGYN 437  
Db 128 AGIANKGQOTREHALLATLVGQKQMVVAINKMDKSTNYSQARYDEIVKEVSSPFIKKIGYN 187  
Qy 438 IKTDVWMPVSGYSGANLKDHDVDPKPCWYTGPTLLLEYLDTMNHVDRHINAPFMLPI--A 495  
Db 188 -PEKVAFPVPSGNGNDMLERSDKWE--WYKGPPTLLLEALDAIVEPKPHDKPLRLPLQDV 244  
Qy 496 AKMKDLGTIVGKIESGHIKKGQSTLLMPNKTAVEIQNIYNETENEVDMAWCGEQVKLRI 555  
Db 245 YKIGGIGTVPVGRVETGIIKPGMVVTFAPAGLSPEVKSVEMHHE-QLPEARPGDNGVFN 303  
Qy 556 KGVVEEDISPGFVLTSFKN-PIKSVTKFVAQIAIVELKSLIAAGFSCVMHVHTAIEEVHI 614  
Db 304 KNVSVKEIKGMVAGDSKNDPPQETEFKFAQVIVLNHPGQIHAGYSPVLDCHTAHIACKF 363  
Qy 615 VKLLHLEKGTNRKSKPPAFAPAKKGMKVIIVLETEAPVVCVETQDYPQLGRFTLRDQ 671  
Db 364 TEIVDKVDRRTGAVVAKEAGTAAVLVKNGDAAMVELTSPRPMCVESFTEYPLGRFAVRDM 423  
Qy 672 GTTIAICKI 680  
Db 424 RQTVAVGVI 432

## RESULT 15

A54760  
translation elongation factor eEF-1 alpha chain - Trypanosoma brucei  
C;Species: Trypanosoma brucei  
C;Date: 28-Oct-1994 #sequence\_revision 21-May-1999 #text\_change 09-Jul-2004  
C;Accession: A54760; C49394  
R;Kaur, K.O.; Ruben, L.  
J. Biol. Chem. 269, 23045-23050, 1994  
A;Title: Protein translation elongation factor-lalpha from Trypanosoma brucei binds cal  
A;Reference number: A54760; MUID:9436499; PMID:8083206  
A;Accession: A54760  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-239, 'TCT', 243-449 <KAU>  
A;Cross-references: UNIPROT:P41166; GB:U10562; NID:g507782; PIDN:AAA57476.1; PID:g507783  
R;Baldauf, S.L.; Palmer, J.D.  
Proc. Natl. Acad. Sci. U.S.A. 90, 11558-11562, 1993  
A;Title: Animals and fungi are each other's closest relatives: congruent evidence from m  
A;Reference number: A49394; MUID:94089672; PMID:8285589  
A;Accession: C49394  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 18-415 <BAL>  
A;Cross-references: GB:L25868; NID:g438909; PIDN:AAA16602.1; PID:g438910  
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homolo  
F;Keywords: calmodulin binding; GTP binding; nucleotide binding; P-loop  
F;8-156/Domain: translation elongation factor Tu homology <ETU>  
F;14-21/Region: nucleotide-binding motif A (P-loop)  
F;153-156/Region: GTP-binding NKXD motif

Query Match 23.3%; Score 836.5; DB 2; Length 449;  
Best Local Similarity 39.9%; Pred. No. 3.2e-36;  
Matches 172; Conservative 88; Mismatches 164; Indels 7; Gaps 5;

Qy 258 KDHVSLIFMGHVDAGKSTMGNNLLYLGTSGVDKRTIEKYEREAKDAGRGQWYLSWVMDTK 317  
Db 5 KVHNNLVVGHVDAGKSTMGNNLLYLGTSGVDKRTIEKYEREAKDAGRGQWYLSWVMDTK 64  
Qy 318 EERNKGKTIIVGKAYFETEKRRYTIIDAPGHMVMVSEMIGGASQADVGLVISARKGEYE 377  
Db 65 AERERGITIDIALWKFFTSKYFTIIDAPGHRDFIKNMITGTSQADCAVLVIASPTGEFE 124  
Qy 378 TGPERGQOTREHALLAKTQGVNKMVNVKMDPTVNMWKERYDOCVSNVSNFLRAIGYN 437  
Db 125 AGISKGQOTREHALLAFTLVGQKQMVVCCNKMDKSTNYSQARYDEIVKEVSAIKKVGYN 184  
Qy 438 IKTDVWMPVSGYSGANLKDHDVDPKPCWYTGPTLLLEYLDTMNHVDRHINAPFMLPI--A 495  
Db 185 VE-KVRFVPSISGQGNMIE--KSEKMPWKYKGPPTLLLEALDMLPEPPVPSKPLRLPLQDV 241  
Qy 496 AKMKDLGTIVGKIESGHIKKGQSTLLMPNKTAVEIQNIYNETENEVDMAWCGEQVKLRI 555  
Db 242 YKIGGIGTVPVGRVETGVMKPGDVTTFAPANVTTEVKSIEMHHE-QLAEATPGDNGVFN 300  
Qy 556 KGVVEEDISPGFVLTSFKN-PIKSVTKFVAQIAIVELKSLIAAGFSCVMHVHTAIEEVHI 614  
Db 301 KNVSVKDIRGNVCGNTKNDPPKAAADFTAQVILNHPGQIHAGYAPVLDCHTSHIACKF 360  
Qy 615 VKLLHLEKGTNRKSKPPAFAPAKKGMKVIIVLETEAPVVCVETQDYPQLGRFTLRDQGT 674  
Db 361 AEIESKIDRSSGKELEKAPKSIKSGDAAIVRMVVPQKPMCVFVENDYAPLGRFAVRDMRQT 420  
Qy 675 IAIGKIVKIAE 685  
Db 421 VAVGIIKAVTK 431

Search completed: July 1, 2005, 18:20:58  
Job time : 42.0283 secs







Qy 296 EREKADAGROGQWYLSWMDTNKEBRNDGKTEIEVGKAYFETEKRRYTTILDAPGHKMYVSEM 355  
Db 110 EREAENKRETWYLSWALDNTQBERDKGKTEVUGRAYFETERKHFTTILDAPGHKSFVPNM 169  
Qy 356 IGASQADVGVLVTSARKGEYETFERGGQTRHALLAKTQGVNKMVWVVMKMDPTVNW 415  
Db 170 IGASQADLAVLVTSARKGEFETGFKGGQTRHAFMGKTAGVKHLVLINKMDPTVNW 229  
Qy 416 SKERYDOCVSNVSNFLRAIGNIKTDVFMVPSVSGANLKHVDHPKCEPMYTGPTLLEY 475  
Db 230 GIERYECKEKLVPFLKKVGFSPKKDTHFMPCSGLTGANIKEQSD--FCPMTYGLPIPY 287  
Qy 476 LDTMNHVDRHINAPFMLPIAAKMDLGTIVBKGIESGHIKKGQSTLLMPNKTAVEIQNIY 535  
Db 288 LNNLPNFRSIDGPIRLPIVDKYGDMGTIVLKGLESIGFKGQQLVMMPNKHNVEVLGIL 347  
Qy 536 NETENEVDMAWCGEQVKLRIRKGVBEEDIISPGFVLTSKPNPIKSVTKVAQIAIVELKSII 595  
Db 348 SD-DTETDFVAPGENLKIRLKGIEEBEILPEFILCDPSNLCHSGRTDFDQVIVIEHKSII 406  
Qy 596 AAGFSCVMHVHTATEEVHIVKLHLKLEKGTNRKSKPPAFAPKGMKVIAVLEAPVCVE 655  
Db 407 CPGYNAVLHIHTCIEEVEITALISLVDKKGSEKSTRPRFVKQDOVCIARLRTAGTICLE 466  
Qy 656 TYQDYPOLGRFTLRDQGTIIAIGKIVKI 683  
Db 467 TFKDFPQMGRTLRDEGKTTAIGKVLK 494

## RESULT 6

US-09-661-468-40  
; Sequence 40, Application US/09661468  
; Patent No. 6376189  
; GENERAL INFORMATION:  
; APPLICANT: FUJIWARA, TSUTOMU  
; APPLICANT: WATANABE, TAKESHI  
; APPLICANT: HORIE, MASATO  
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN  
; FILE REFERENCE: Q-53599  
; CURRENT APPLICATION NUMBER: US/09/661,468  
; CURRENT FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: 09/055,699  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: 08/820,170  
; PRIOR FILING DATE: 1997-03-19  
; PRIOR APPLICATION NUMBER: JP 63410/1996  
; PRIOR FILING DATE: 1996-03-19  
; PRIOR APPLICATION NUMBER: JP 69163/1997  
; PRIOR FILING DATE: 1997-03-05  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 499  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-661-468-40

Query Match 36.4%; Score 1307.5; DB 3; Length 499;  
Best Local Similarity 45.4%; Pred. No. 3.1e-106;  
Matches 251; Conservative 94; Mismatches 146; Indels 17; Gaps 5;

Qy 178 ETKEPTKPTKVEBPVKKEEPVQTEKTEKSELPKVEDLKISESTHNTNNAVTSADA 237  
Db 2 ELSEFPVVEGEVE-----MALESWEHSKEVSEAP---GGSGSDSGPPEESQGE 49  
Qy 238 LIKEQEE--EYDDEVNDMFGKDHVSLIFMGHVDAKSTMGGLLYLTGSDVKRTIEKY 295  
Db 50 MMEKEIRKSKSVIVPSGAPKKEHVNVFVGHVDAKSTIGGIMFLTGMADKRTIEKY 109  
Qy 296 EREKADAGROGQWYLSWMDTNKEBRNDGKTEIEVGKAYFETEKRRYTTILDAPGHKMYVSEM 355  
Db 110 EREAENKRETWYLSWALDNTQBERDKGKTEVUGRAYFETERKHFTTILDAPGHKSFVPNM 169

Qy 356 IGASQADVGVLVTSARKGEYETFERGGQTRHALLAKTQGVNKMVWVVMKMDPTVNW 415  
Db 170 IGASQADLAVLVTSARKGEFETGFKGGQTRHAFMGKTAGVKHLVLINKMDPTVNW 229  
Qy 416 SKERYDOCVSNVSNFLRAIGNIKTDVFMVPSVSGANLKHVDHPKCEPMYTGPTLLEY 475  
Db 230 GIERYECKEKLVPFLKKVGFSPKKDTHFMPCSGLTGANIKEQSD--FCPMTYGLPIPY 287  
Qy 476 LDTMNHVDRHINAPFMLPIAAKMDLGTIVBKGIESGHIKKGQSTLLMPNKTAVEIQNIY 535  
Db 288 LNNLPNFRSIDGPIRLPIVDKYGDMGTIVLKGLESIGFKGQQLVMMPNKHNVEVLGIL 347  
Qy 536 NETENEVDMAWCGEQVKLRIRKGVBEEDIISPGFVLTSKPNPIKSVTKVAQIAIVELKSII 595  
Db 348 SD-DTETDFVAPGENLKIRLKGIEEBEILPEFILCDPSNLCHSGRTDFDQVIVIEHKSII 406  
Qy 596 AAGFSCVMHVHTATEEVHIVKLHLKLEKGTNRKSKPPAFAPKGMKVIAVLEAPVCVE 655  
Db 407 CPGYNAVLHIHTCIEEVEITALISLVDKKGSEKSTRPRFVKQDOVCIARLRTAGTICLE 466  
Qy 656 TYQDYPOLGRFTLRDQGTIIAIGKIVKI 683  
Db 467 TFKDFPQMGRTLRDEGKTTAIGKVLK 494

## RESULT 7

US-09-976-165-40  
; Sequence 40, Application US/09976165  
; Patent No. 6562947  
; GENERAL INFORMATION:  
; APPLICANT: FUJIWARA, TSUTOMU  
; APPLICANT: WATANABE, TAKESHI  
; APPLICANT: HORIE, MASATO  
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN  
; FILE REFERENCE: Q-53599  
; CURRENT APPLICATION NUMBER: US/09/976,165  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/565,538  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: 09/055,699  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: 08/820,170  
; PRIOR FILING DATE: 1997-03-19  
; PRIOR APPLICATION NUMBER: JP 63410/1996  
; PRIOR FILING DATE: 1996-03-19  
; PRIOR APPLICATION NUMBER: JP 69163/1997  
; PRIOR FILING DATE: 1997-03-05  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 499  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-976-165-40

Query Match 36.4%; Score 1307.5; DB 4; Length 499;  
Best Local Similarity 49.4%; Pred. No. 3.1e-106;  
Matches 251; Conservative 94; Mismatches 146; Indels 17; Gaps 5;

Qy 178 ETKEPTKPTKVEBPVKKEEPVQTEKTEKSELPKVEDLKISESTHNTNNAVTSADA 237  
Db 2 ELSEFPVVEGEVE-----MALESWEHSKEVSEAP---GGSGSDSGPPEESQGE 49  
Qy 238 LIKEQEE--EYDDEVNDMFGKDHVSLIFMGHVDAKSTMGGLLYLTGSDVKRTIEKY 295  
Db 50 MMEKEIRKSKSVIVPSGAPKKEHVNVFVGHVDAKSTIGGIMFLTGMADKRTIEKY 109  
Qy 296 EREKADAGROGQWYLSWMDTNKEBRNDGKTEIEVGKAYFETEKRRYTTILDAPGHKMYVSEM 355  
Db 110 EREAENKRETWYLSWALDNTQBERDKGKTEVUGRAYFETERKHFTTILDAPGHKSFVPNM 169



Qy 356 IGGASQADVGLVISARKGEYETGPERGGOTREHALLAKTQGVNKNVNVVVKMDPTVNW 415  
Db 170 IGGASQADALVLVISARKGEFETFEKGGQREHAMFGKTAGVXHLIVLIVNKMDPTVNW 229  
Qy 416 SKERYDQCVSNVSNFLRAIGNIKITDVVFMVPSVSGYSGANLKHVDHPKPCPYTGTLLLEY 475  
Db 230 GIEREYBECKELVFLKVKVSPKDIHFMCISGLTGANIKEQSD--FCPYWTGLPTPY 287  
Qy 476 LDTWNHVDHINAFMLPIAAKMDLGTIVGKIESGHKKGQSTLLMPNKTAVEIQNIY 535  
Db 288 LNNLPFNFRSDGPTIRLPVVDKYDMGTIVLKGLESIGFQGGQQLVMMPNKHNEVLGIL 347  
Qy 536 NETENEDVMAMCGOVKLRIKGVSEEDISPGFVLTSKPNPKSVTKFVAQIAIIVELKSI 595  
Db 348 SD-DTETDFVAPGNNKIRLKGIBEEILPELFIILCDPSNLCHSGRTFDVQIVIEHKSII 406  
Qy 596 AAGFSCVNHVHTAIEEVHIVKLLHLEKGTNRKSKPPAFKGMKVIATVLEAPVCVE 655  
Db 407 CPGINAVLHIHTCIEEVEITALISIVDKSGEKSRTPRFVKQDOVCIARLRTAGTICLE 466  
Qy 656 TYQDYPQLGRFTLRDQGTIIAGKIVKI 683  
Db 467 TFKDFPQMGRTLRDEGTIIAGKIVKL 494

## RESULT 8

US-09-248-796A-19828  
; Sequence 19828, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR FILING DATE: 1998-02-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 19828  
; LENGTH: 276  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-19828

Query Match 29.8%; Score 1072.5; DB 4; Length 276;  
Best Local Similarity 70.3%; Pred. No. 5.7e-86;  
Matches 194; Conservative 40; Mismatches 41; Indels 1; Gaps 1;  
Qy 408 MDDPTVWNSKERYDQCVSNVSNFLRAIGNIKITDVVFMVPSVSGYSGANLKHVDHPKPCPY 467  
Db 1 MDDSTVWNSKERYDQCVSNVSNFLRAIGNIKITDVVFMVPSVSGYSGANLKHVDHPKPCPY 59  
Qy 468 TGPTLLBYLDTMNHVDHINAFMLPIAAKMDLGTIVGKIESGHKKGQSTLLMPNK 527  
Db 60 DGPSLLEYLDNMDTMRKINGPFMMVPSGKMDLGTIVGKIESGHKKGQSTLLMPNK 119  
Qy 528 AVELQNIYNETENEDVMAMCGOVKLRIKGVSEEDISPGFVLTSKPNPKSVTKFVAQIA 587  
Db 120 PIEVLTIFNETEQCDTAFSGEQLRIKIGIEEDLQFGYVLTSPKPNPKSVTKFVAQIA 179  
Qy 588 IVELKSIAGFSCVMHVTAEIEVHIVKLLHLEKGTNRKSKPPAFKGMKVIATVLE 647  
Db 180 IVELKSIILNSGFCVMHVTAEIEVHIVKLLHLEKGTNRKSKPPAFKGMKVIATVLE 239  
Qy 648 TEAPVCVETYQDYPQLGRFTLRDQGTIIAGKIVKI 683  
Db 240 VGLVCAETKYDYPQLGRFTLRDQGTIIAGKIVKL 275

## RESULT 9

US-09-248-796A-19819  
; Sequence 19819, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR FILING DATE: 1998-02-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 19819  
; LENGTH: 460  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-19819

Query Match 23.1%; Score 831; DB 4; Length 460;  
Best Local Similarity 39.0%; Pred. No. 2.3e-64;  
Matches 173; Conservative 87; Mismatches 160; Indels 24; Gaps 9;  
Qy 258 KDHVSLIPMGHVDAGKSTMGNNLLYLTGSDVDKRTIEKYERAKDAGROGWYLSVWMDTNK 317  
Db 7 KTHVNVVIVGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKAEALGKSGFYAWVLDK 66  
Qy 318 EERNKGKTIEVGKAYFETEKRRYVLTIDAPGHKMYSEMIGCASOADVGLVISARKGEYE 377  
Db 67 ABERGKITIDIALWKFPKPYHVTVIDAPGHRDFIKNMITGTSQADCAILIIAGTGGEFE 126  
Qy 378 TGFERGGQTRHALLAKTQGVNKNVNVVVKMDPTVWNSKERYDQCVSNVSNFLRAIGNY 437  
Db 127 AGTSKQGTREHALLAYTLGVKQLIVAVNKM--SVKMDKURFEIILKETSNFVKKGVN 184  
Qy 438 IKTDVPMVPSVSGYSGANLKHVDHPK-BCPYW-----TGPTLLBYLDTMNHVDR 484  
Db 185 PKT-VFPVPISGMNGDNM--IEPSTNCPWYKGEKETSKGKVTGKTILLEAIDAIEPPT 240  
Qy 485 HINAPFMLPI--AAKMDLGTIVGKIESGHKKGQSTLLMPNKTAVEIQNIYNETENEV 542  
Db 241 PTDKPLRLQDVYKIGGIVPVGRVETGIIKAGMVVTFAPAGVTTVEKSVEMHHE--QL 299  
Qy 543 DMAMCGOVKLRIKGVSEEDISPGFVLTSKPN-PIKSVTKFVAQIAIIVELKSIAGFSC 601  
Db 300 AEGVPGDVGPNVGNVSVKSEIRRGVNCDSKNDPPKGCDSFNAQVIVLHNFQGISAGYSP 359  
Qy 602 VMHVTAEIEVHIVKLLHLEKGTNRKSKPPAFKGMKVIATVLEAPVCVETYQDYP 661  
Db 360 VLDCHTAHIAKCFDTLVEKIDRRTGKLEENPKFVSGDAAIKVMVPTKPMCVBEAFTDYP 419  
Qy 662 QLGRFTLRDQGTIIAGKIVKIAE 685  
Db 420 PLGRFAVRDMRQTAVAG-VIKSVE 442

## RESULT 10

US-08-299-351-1  
; Sequence 1, Application US/08299351  
; Patent No. 5576186  
; GENERAL INFORMATION:  
; APPLICANT: Stetler, Dean A.  
; TITLE OF INVENTION: DIAGNOSIS AND MONITORING OF  
; TITLE OF INVENTION: RHEUMATOLOGICAL DISEASES BY DETECTION OF ANTI-EP-1alpha  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS  
; STREET: 1400 Mercantile Bank Tower, 1101 Walnut St.  
; CITY: Kansas City  
; STATE: Missouri



```
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9570
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9570

Query Match      22.2%; Score 797.5; DB 4; Length 469;
Best Local Similarity 38.5%; Pred. No. 2.1e-61;
Matches 170; Conservative 88; Mismatches 156; Indels 25; Gaps 8;

Qy 258 KDHSLLIPMGHVDAGKSTMGNNLLYLTGSDVKRTIEKYERAKDAGROGWLSWMDTNK 317
Db 12 KTHNIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKEKEAAEMGKSPKYAWVLDK 71

Qy 318 ERNDGKTIEVGKAYFETEKERYTILDAPGHMYYSEMIGGASQADVGVLVISARKGEY 377
Db 72 AERERGITIDISLWKFTSKYVVTIIDAPGHRDFIKNMITGTSQADCAVLIVAAGVG 131

Qy 378 TGFERGGOTREHALLAKTQGVNKMVVVNMKDDPTVNMKERYDOCVSNVNFLEAIGY 437
Db 132 AGISKNGOTREHALLAYTLGVKQLIVGNKMDSTPEPPYSQRYEIEVKEVSTYIKIG 191

Qy 438 IKTDVFMFVPSGYSGANLKDHVDPK-ECPPWY-----TGPTLLEYLDTMNHVDR 484
Db 192 PDT-VAFVPIISGNGDNM--LEPSANMPWFKGMKVTCKDGNASGTTILLEALDCILP 247

Qy 485 HINAPFMLPI--AAKMDLGTIVGKIESGHIKKGQSTLLMPNKTAVBIONI--YNETEN 540
Db 248 PTDKPLRLPLQDVYKIGIGTVPVGRVETGLKPGMVVTFAPVNVVTTTEVKSVMHEALS 307

Qy 541 EVDAMCGEQVKLRKIGVEEEDISPGFVLTSPKN-PIKSVTKFVAQIAIVELKSLIAAG 599
Db 308 E---ALPGDNVGFNVKNSVDRGNVAGSKNDPPMEAAAGFTAQVILNHPGQISAGY 364

Qy 600 SCVMHVHTAIEVHIVKLLHLEKGTNRKSKPPAFKGMKVIKAVLETEAPVCVETQD 659
Db 365 APVLDCHTAHTACKFAELKEKIDRRSGKLEDDGPKFLKSGDAAIVDMVPGKPMCVES 424

Qy 660 YPOLGRFTRLDQGTIIAGKI 680
Db 425 YPPLGRFAVRDMQTAVGV 445

RESULT 13
US-09-949-016-9571
; Sequence 9571, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9571
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9571
```

```
Query Match      22.2%; Score 797.5; DB 4; Length 469;
Best Local Similarity 38.5%; Pred. No. 2.1e-61;
Matches 170; Conservative 88; Mismatches 156; Indels 25; Gaps 8;

Qy 258 KDHSLLIPMGHVDAGKSTMGNNLLYLTGSDVKRTIEKYERAKDAGROGWLSWMDTNK 317
Db 12 KTHNIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKEKEAAEMGKSPKYAWVLDK 71

Qy 318 ERNDGKTIEVGKAYFETEKERYTILDAPGHMYYSEMIGGASQADVGVLVISARKGEY 377
Db 72 AERERGITIDISLWKFTSKYVVTIIDAPGHRDFIKNMITGTSQADCAVLIVAAGVG 131

Qy 378 TGFERGGOTREHALLAKTQGVNKMVVVNMKDDPTVNMKERYDOCVSNVNFLEAIGY 437
Db 132 AGISKNGOTREHALLAYTLGVKQLIVGNKMDSTPEPPYSQRYEIEVKEVSTYIKIG 191

Qy 438 IKTDVFMFVPSGYSGANLKDHVDPK-ECPPWY-----TGPTLLEYLDTMNHVDR 484
Db 192 PDT-VAFVPIISGNGDNM--LEPSANMPWFKGMKVTCKDGNASGTTILLEALDCILP 247

Qy 485 HINAPFMLPI--AAKMDLGTIVGKIESGHIKKGQSTLLMPNKTAVBIONI--YNETEN 540
Db 248 PTDKPLRLPLQDVYKIGIGTVPVGRVETGLKPGMVVTFAPVNVVTTTEVKSVMHEALS 307

Qy 541 EVDAMCGEQVKLRKIGVEEEDISPGFVLTSPKN-PIKSVTKFVAQIAIVELKSLIAAG 599
Db 308 E---ALPGDNVGFNVKNSVDRGNVAGSKNDPPMEAAAGFTAQVILNHPGQISAGY 364

Qy 600 SCVMHVHTAIEVHIVKLLHLEKGTNRKSKPPAFKGMKVIKAVLETEAPVCVETQD 659
Db 365 APVLDCHTAHTACKFAELKEKIDRRSGKLEDDGPKFLKSGDAAIVDMVPGKPMCVES 424

Qy 660 YPOLGRFTRLDQGTIIAGKI 680
Db 425 YPPLGRFAVRDMQTAVGV 445

RESULT 14
US-09-309-572-10
; Sequence 10, Application US/09309572
; Patent No. 6440730
; GENERAL INFORMATION:
; APPLICANT: Heinrich-Pette-Institut
; TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV
; FILE REFERENCE: P50489
; CURRENT APPLICATION NUMBER: US/09/309,572
; CURRENT FILING DATE: 1999-05-11
; EARLIER APPLICATION NUMBER: DE 198 56 463
; EARLIER FILING DATE: 1998-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: elongation factor EF-1-alpha
US-09-309-572-10

Query Match      22.2%; Score 796.5; DB 4; Length 462;
Best Local Similarity 38.3%; Pred. No. 2.5e-61;
Matches 169; Conservative 89; Mismatches 156; Indels 25; Gaps 8;

Qy 258 KDHSLLIPMGHVDAGKSTMGNNLLYLTGSDVKRTIEKYERAKDAGROGWLSWMDTNK 317
Db 5 KTHNIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKEKEAAEMGKSPKYAWVLDK 64

Qy 318 ERNDGKTIEVGKAYFETEKERYTILDAPGHMYYSEMIGGASQADVGVLVISARKGEY 377
Db 65 AERERGITIDISLWKFTSKYVVTIIDAPGHRDFIKNMITGTSQADCAVLIVAAGVG 124

Qy 378 TGFERGGOTREHALLAKTQGVNKMVVVNMKDDPTVNMKERYDOCVSNVNFLEAIGY 437
Db 132 AGISKNGOTREHALLAYTLGVKQLIVGNKMDSTPEPPYSQRYEIEVKEVSTYIKIG 191
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Db 125 AGISKNGQTRHALLAYTLGVKQLIVGNKMDSTPEPPYSQRYBEIVKEVSTYIKKIGYN 184  
Qy 438 IKTDVFMFVSGYSGANLKHVDPK-ECPLY-----TGPTLLEYLDTMNHVDR 484  
Db 185 PDT-VAFVPISGWNGDNM---LEPSANMPFKGWKVTNRKDGNSGTTLLLEALDCILPPT 240  
Qy 485 HINAPFMLPI--AAKMDLGTIVGKTESGHIKKQSTLLMPNKTAVEIQNI--YNETEN 540  
Db 241 PTDKPLRLPLQDVYKIGGIGTFVGRVETGVLKPGWVTFAPVNVVTEVKSVEHHEALS 300  
Qy 541 EVDWAMCGEQVKLRKIGVEEBDISPGFVLTSPPKN-PIKSVTKFVAQIAIIVELKSIIAAGF 599  
Db 301 E---ALPGDNVGNVKNVSKDVRGNAVAGDSKNDPPMEAAGFTAQVVIILNHPQISAGY 357  
Qy 600 SCVMHVHTAIEEVHIVKLLHLEKGTNRKSKPPAPAKKGMKVIAVLETAAPVCVETYQD 659  
Db 358 APVLDCHTAHIAACKFAELKEKIDRRSGKLEDPKFLKSGDAAIVDMVPGKPMCVESFSD 417  
Qy 660 YPOLGRFTLRDQGTIAIGKI 680  
Db 418 YPPLGRFAVRDMRQTVAAGVI 438

## RESULT 15

US-09-718-096-10  
; Sequence 10, Application US/09718096  
; Patent No. 6589763  
; GENERAL INFORMATION:  
; APPLICANT: Von Laer, Meike-Dorothee  
; TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV  
; FILE REFERENCE: 35-195  
; CURRENT APPLICATION NUMBER: US/09/718,096  
; CURRENT FILING DATE: 2000-11-22  
; PRIOR APPLICATION NUMBER: DE 19856463.5  
; PRIOR FILING DATE: 1998-11-26  
; PRIOR APPLICATION NUMBER: EP 99250415.9  
; PRIOR FILING DATE: 1999-11-25  
; PRIOR APPLICATION NUMBER: US 09/309,572  
; PRIOR FILING DATE: 1999-05-11  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: elongation factor EF-1-alpha  
US-09-718-096-10

Query Match 22.2%; Score 796.5; DB 4; Length 462;  
Best Local Similarity 38.3%; Pred. No. 2.5e-61;  
Matches 169; Conservative 89; Mismatches 158; Indels 25; Gaps 8;  
Qy 258 KDVSLIFMGHVDAGKSTMGNNLLYLTGSVDKRTIEKYERAKDAGRGQWYLSWVMDTNK 317  
Db 5 KTHINIVVIGHVDGSKSTTTGHLIYKCGIDKRTIEKEAEAKGSKFYANVLDKX 64  
Qy 318 EERNKGKTIIEVGKAYFETEKERYTILDPAGHKMVTSEMIGGASQADVGLVVISARKGEYE 377  
Db 65 AERERGITIDISLWKFTSKYVVTIIDAPGHRDFIKNMITGTSQADCAVLIVAAAGVGEFE 124  
Qy 378 TGFPERGGQTRHALLAKTQGNKMWVNNKMDPTVWNSKERYDQCVSNUSNFLRAIGYN 437  
Db 125 AGISKNGQTRHALLAYTLGVKQLIVGNKMDSTPEPPYSQRYBEIVKEVSTYIKKIGYN 184  
Qy 438 IKTDVFMFVSGYSGANLKHVDPK-ECPLY-----TGPTLLEYLDTMNHVDR 484  
Db 185 PDT-VAFVPISGWNGDNM---LEPSANMPFKGWKVTNRKDGNSGTTLLLEALDCILPPT 240  
Qy 485 HINAPFMLPI--AAKMDLGTIVGKTESGHIKKQSTLLMPNKTAVEIQNI--YNETEN 540  
Db 241 PTDKPLRLPLQDVYKIGGIGTFVGRVETGVLKPGWVTFAPVNVVTEVKSVEHHEALS 300

Qy 541 EVDWAMCGEQVKLRKIGVEEBDISPGFVLTSPPKN-PIKSVTKFVAQIAIIVELKSIIAAGF 599  
Db 301 E---ALPGDNVGNVKNVSKDVRGNAVAGDSKNDPPMEAAGFTAQVVIILNHPQISAGY 357  
Qy 600 SCVMHVHTAIEEVHIVKLLHLEKGTNRKSKPPAPAKKGMKVIAVLETAAPVCVETYQD 659  
Db 358 APVLDCHTAHIAACKFAELKEKIDRRSGKLEDPKFLKSGDAAIVDMVPGKPMCVESFSD 417  
Qy 660 YPOLGRFTLRDQGTIAIGKI 680  
Db 418 YPPLGRFAVRDMRQTVAAGVI 438

Search completed: July 1, 2005, 18:39:39  
Job time : 58.3582 secs



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Qy 176 SAETK--EPTKEPTKVBEPVKBKBPVQTEBTEKSELPKVEDLKISESTHNTNNANVT 233
Db 155 KKEKKAEPKEQSKKEEP-KREGTPPAAAKDEKEDLPLEKELKIKE---EQAAANAS 210
Qy 234 SADALIKEQEEVEVDVNDMFGGKHVSIIIFMGHVDAGKSTMGNNLLYLTGSDVKRTIE 293
Db 211 GADSLIKEQEEVEVDVNDMFGGKHWSIIFMGHVDAGKSTMGNNLYMTGSDVKRTVE 270
Qy 294 KYEREAADAGROGHYLSWMDTNKEERNDDGKTIEVGKAYFETEKRRYTIILDAPGHKMYVS 353
Db 271 KYEREAADAGROGHYLSWMDTNREERDDGKTIEVGGRAYFETEKRRYTIILDAPGHKMYVS 330
Qy 354 EMIGGASQADVGLVVISARKGEYETGFERGGQTRHALLAKTQGVNKMVVVNNKMDDPV 413
Db 331 EMIGGASQADVGLVVISARKGEYETGFERGGQTRHALLAKTQGVNKLITVNNKMDDPV 390
Qy 414 NWSKERYDQCVSNVSNFLRAIGNIKTDVVFMFVPSYSGANLKDHDVDPKPCPWYTGPTLL 473
Db 391 NWSKERYDQCVSNLNFELKALGYNVKEVFMFVPSYSGAGLGRVDPKPCPWYDGPALL 450
Qy 474 EYLDTMNHDHINAPFMLPIAAKMDLGTIVVEKIESGHIKKGQSTLLMPNKTAVBIQN 533
Db 451 EYMDNMSHVRDMNAPFMLPIAAKORDMGITVEGKIESGHIRKGHSTLLMPNKIPVBION 510
Qy 534 IYNETENEVDMAKGEQVKLRIKGVBEEDISPGFVLTSKPNPIKSVTKFVAQIAIVELKS 593
Db 511 IYNETENEVDMAKGEQVKLRIKGVBEEDISPGFVLTSKPNPVKNVTRFVAQIAIVELKS 570
Qy 594 IIAAGFSCVMHVHTAIEBVHIVKLLHLEKGTNRKSKPPAFKMGKMKVIAVLETEAPVC 653
Db 571 ILSGFGFSCVMHVHTAIEBVHIVKLLHLEKGTNRKSKPPAFKMGKMKVIAVLETERPVC 630
Qy 654 VETYQDPQLGRFTLRDQGTIIAGIKVKTAB 685
Db 631 VETYQDPQLGRFTLRDQGTIIAGIKVKTAB 662
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## RESULT 2

```
US-10-732-923-17486
; Sequence 17486, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 17486
; LENGTH: 712
; TYPE: PRT
; ORGANISM: Candida maltosa
US-10-732-923-17486
```

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Query Match 65.9%; Score 2367; DB 17; Length 712;
Best Local Similarity 67.7%; Pred. No. 3.7e-145;
Matches 485; Conservative 61; Mismatches 108; Indels 62; Gaps 16;

Qy 4 SNOGNNQNYQYYSQ-NGNQOQGNRRYQGYQAYNAQAQPA-GGYQYQNYQYSGYQCGGYQ 61
Db 22 SKQPQQQQQQQQQYFNPNOQAQFVPTGGYQQQFQFQOQQQYQQN---YTCQAAGGYQ 78
Qy 62 Q-YNPDAGYQQYQNPQGGYQ-Q-YNPQGGYQQQFNPQGGRGNYKNFNTNNLQGYQA---- 115
Db 79 QYNNRRGYQQYNNRRGYQQYNNRRGYQQOQQQQ-----YQAYNPNQYGGYQAYNPQ 133
Qy 116 ---GFQPSQSGMSLNDFOKQ---OKQAA---PKPKTKLKVSSSGIKLANATKVGKT-KPA 166
Db 134 QQQQQQQQSQSGMSLADFQKQAEQQAQSLNKPAPVKTKLKLASSSGIKLANATKVKYDTAKPA 193
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Qy 167 ESDK-----KEEKSAETKEPTKEPTKV-----BEPVKEKBPVQTEBTEKTE 207
Db 194 ASKEASPAPKDEASAE-PEAKKESPTVPASSPAPAAADSTPAPVKKESTPT----- 245
Qy 208 EKSELPKVEDLKISESTHNTNNANVTADALIKEQEEVEVDVNDMFGGKHVSIIIFMG 267
Db 246 ----PSV-----ASKAPVVSASVVTADALAKEQEEVEVDVNDMFGGKHVSIIIFMG 296
Qy 268 HVDAGKSTMGNNLLYLTGSDVKRTIEKYEREAADAGROGHYLSWMDTNKEERNDDGKTIE 327
Db 297 HVDAGKSTMGNNLLYLTGSDVKRTIEKYEREAADAGROGHYLSWMDTNKEERNDDGKTIE 356
Qy 328 VGKAYFETEKRRYTIILDAPGHKMYVSEMIIGASQADVGLVVISARKGEYETGFERGGQTR 387
Db 357 VGKAYFETDKRRYTIILDAPGHKMYVSEMIIGASQADVGLVVISARKGEYETGFERGGQTR 416
Qy 388 EHALLAKTQGVNKMVVVNNKMDDPVTVNWSKERYDQCVSNVSNFLRAIGNIKTDVVFMFV 447
Db 417 EHALLAKTQGVNKKIIVVNNKMDDPVTVNWSKERYDQCVSNVSNFLRAIGNIKTDVVFMFV 475
Qy 448 SGYSGANLKDHDVDPKPCPWYTGPTLLLEYLDTMNHVDHINAPFMLPIAAKMDLGTIVVEG 507
Db 476 SGYTAGLKDORVAPKDCPWTYEGSPSLLEYLNDMTMKKINGPMPVSGKMDLGTIVVEG 535
Qy 508 KIESGHIKKGQSTLLMPNKTAVBIQNIYNETENEVDMAKGEQVKLRIKGVBEEDISPGF 567
Db 536 KIESGHVVKGTNLLMPNKTPEVLTINYNETEQEADTAPSGEQVRLKIKGVBEEDLQPY 595
Qy 568 VLTSKPNPIKSVTKFVAQIAIVELKSIIAAGFSCVMHVHTAIEBVHIVKLLHLEKGTNR 627
Db 596 VLTSKPNPVKTVTKFEAQIAIVELKSIILNSGFCVWMLHTAIEBEVKEFVELKHLKGTNR 655
Qy 628 KSKKPPAFKMGKMKVIAVLETEAPVCVETQYDPQLGRFTLRDQGTIIAGIKVKTAB 683
Db 656 KSKKPPAFKMGKMKIIAILEVSEPVCAETKYDYPQLGRFTLRDQGTIIAGIKVKTAB 711
```

## RESULT 3

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US-10-032-585-7274
; Sequence 7274, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7274
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7274
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Query Match 65.3%; Score 2347.5; DB 14; Length 721;
Best Local Similarity 64.8%; Pred. No. 6.9e-144;
Matches 471; Conservative 79; Mismatches 118; Indels 59; Gaps 17;

Qy 8 NNQONTQYQY-----SQNGN---OQOQGNRRYQGYQAYNAQAQ-----PAGGY--YQNYQ 50
Db 2 SDOQNTODQLSGAVANASLNGDSKQOQOQOQOQOQOQYNNPNAQAQSFVPGGYQQFQFQ 61
Qy 51 GYSGYQQ-QGYQOYNP-DAGYQQOYNPQGGYQ-Q-YNPQGGYQQOQFNPQGGRGNYKNFNYN 107
Db 62 PQOQOQOQGYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 118
Qy 108 NNQGYQA-QFQP-----SQQMSLNDFOKQ---OKQAA---PKPKTKLKVSSSGIKLA 155
Db 119 QYQGYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 178
```







US-10-369-493-22730

Query Match 46.7%; Score 1679.5; DB 15; Length 690;  
Best Local Similarity 51.4%; Pred. No. 1.6e-100;  
Matches 332; Conservative 109; Mismatches 148; Indels 57; Gaps 15;

QY 68 GYQQQYNPQGG--YQYNPQGGYQQQFNPQGGRGYKFNFNNNLQYQAGFQPOQSGMS 125  
DB 74 GFVPVNNIAGGYPYAYQYTGQ-----QNSNSPHPTKSYQQYYQ-KPTGNT 117  
QY 126 LN-----DFQOQQAAPKPK-----KTLKL-----VSSSGIKLANATKK 160  
DB 118 VDDEKSRVPDFSKKSFVPPKPAIPKGVLSLGGNTSAPKSTPKPISISLGGTKAPTIXP 177  
QY 161 VGTQPAESDKKEEKSASAEKTEKPTKVBEVPKKEKPVQTEKTEKSELKPKVEDLKI 220  
DB 178 AA--PAAQSKTETPAKPVTSSTKETAAPP--QETP--TKSADAELAKTPSAPAAAL 230  
QY 221 SESTHTNNANVTSADALIKOESEEVDDDEVNDMEFGGDHVSLLIFMGHVDAGKSTMGNNL 280  
DB 231 KKAABAABPATVTE--DA--TDLQNEVDQELLKDMY-GKEHVNIVFIHVDAGKSTLGGNI 286  
QY 281 LYLTPAGHMYVSEMIIGASQADVGVLVI SARKGEYETGFERGGQTRHALLAKTQGVNK 340  
DB 287 LFLTCGVNDKRTWEKIEREAKGAGKESWLSWALDSTSEEREKGTVEVGRAYFETEHRRP 346  
QY 341 TILDAPGHMYVSEMIIGASQADVGVLVI SARKGEYETGFERGGQTRHALLAKTQGVNK 400  
DB 347 SLLDAPGHKGYVNNINGASQADIGVLVTSARRGEFEAGFERGGQTRHALLARTQGINH 406  
QY 401 MVVNNKMDPTVNNKERYDOCVSNVSNFLRAI-GYNIKTVDVWMPVSGYSGANLKHV 459  
DB 407 LVVNNKMDPTVNNKERYDOCVSNVSNFLRAI-GYNIKTVDVWMPVSGYSGANLKHV 466  
QY 460 DPKECPWTGPTLLBYLDMHVDHINAPFMPPIAAKMDLGTIVGKIESGHIKKGOS 519  
DB 467 DSSVCPTQGSLLBYLSWTHLERKVNAPFIMPIASKYKDLGTILEKIEAGSIKONS 526  
QY 520 TLLMPNKTAVEIQNTYNETENEVDMMAMCGEQVKLRIGKVEBEDISPGFVLTSPPKNPIKSV 579  
DB 527 VLWMPINQTLVTAIYDEADEEISSICDQVRLVRVG-DDSDVGTQVLTSTKQPVHAT 585  
QY 580 TKFVAQIAIIVELKSIIAAGFCVMMVHTAIBEVHIVKLLHLEKGTNRKSKPPAFAPAKG 639  
DB 586 TRFIAQIAIILPSLITLGYSCWMIHTAVEEVSFAKLLHLKLDK-TNRKSKPPMPFATKG 644  
QY 640 MKVIATVLEAPVCVETQDYPQLGRFTLRDQGTIIAIGKIVKIAE 685  
DB 645 MKIIAELETQTPVCMERFEDQYMGRTLRDQGTIIAIGKIVKIAE 690

## RESULT 8

US-10-320-797-3284  
; Sequence 3284, Application US/10320797  
; Publication No. US20040014955A1  
; GENERAL INFORMATION:  
; APPLICANT: Eroshkin, Alexey M.  
; APPLICANT: Zamudio, Carlos  
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND METHODS OF USE  
; FILE REFERENCE: 10182-021-999  
; CURRENT APPLICATION NUMBER: US/10/320,797  
; CURRENT FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: 60/341,261  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 3361  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3284  
; LENGTH: 720  
; TYPE: PRT  
; ORGANISM: Cryptococcus neoformans  
US-10-320-797-3284

Query Match 46.1%; Score 1658; DB 15; Length 720;

Best Local Similarity 48.1%; Pred. No. 4.2e-99;  
Matches 335; Conservative 97; Mismatches 176; Indels 88; Gaps 13;

QY 38 QAQPAAGGYQNYGYSGYQQGGYQQYNPQGGYQQYNPQGGYQQYNPQGGYQQYNPQGG 97  
DB 48 QQQPDPY-----GQQQGGYQYQ-----YQYQQGGYQYQYQYQYQYQYQYQYQYQY 86  
QY 98 RGNYNKFNFNNNLQYQA-----GFQPOSQMGSLNDFQKQQAAPKPKTKLKLVS 148  
DB 87 -----QGYVPVPGAPGAPRAYQP--PQARNVQGFQPPSFSSPAPPDPTKAPA 132  
QY 149 SSGIKLA-----NATKVGTKPAESDKKEEKSASAEKTEKPTKVBEVPKKEE--KPQV 201  
DB 133 GKPVLSLSTGGGAPK---AAPSLSIEKESASSKSPKPAAPTTPKPADAPAKSEASAPVS 189  
QY 202 TEEKTEEKSELPKVEDLK-----ISESTHTNNANVTS---AD 236  
DB 190 AAEKKAERK-VPLTSDAQGVVAETSAAKSPAKSGASTPVATVSTSTTNFSKVSANDAE 248  
QY 237 ALIKQESEEVDDDEVNDMEFG-----KDHVSLIFMGHVDAGKSTMGNNLILYLTGSVDK 289  
DB 249 AIYREQ-NLAGDAALRDLYGENVDNIKSHLNIIFTGHVDAGKSTMGQQLLYLTGAVDK 307  
QY 290 RTIEKYEREKADAGQGHVLSWMDTNKEERNDGKTIIEVGKAYFETEKERYTILDAPGHK 349  
DB 308 RTMEKYEQEAKAAGRETWYLSWALDSGKEERAKGTVEVGRAYFSEKRRYITILDAPGHK 367  
QY 350 MYVSEMIIGASQADVGVLVI SARKGEYETGFERGGQTRHALLAKTQGVNKMVVNNKMD 409  
DB 368 TVVSMISGAQAQDVALLVLSARKGEFETGFEREGQTRHALLIKNGINKLIVVNNKMD 427  
QY 410 DPTVNNKERYDOCVSNVSNFLRAIIGYNIKTVDVWMPVSGYSGANLKHVDPEKCPWTG 469  
DB 428 DTTQWMDKGRYDEITTKITPFLKAVGFNPKDITFIPVSAQIGENKMDKRVKKIAPWMDG 487  
QY 470 PTLLEYLDMHVDHINAPFMPPIAAKMDLGTIVGKIESGHIKKGOSTLLMPNKTAIV 529  
DB 488 PSLLEHLDNIMDRINAPFMPPISEKYNELGTVMVGKIESGHVKKGDTLLMPNKHV 547  
QY 530 EIQNIYNETENEVDMMAMCGEQVKLRIGKVEBEDISPGFVLTSPPKNPIKSVTKFVAQIAIV 589  
DB 548 EVTGIFQSQSEMDMAFCGDNIWRISGVSRDITPGFVLTSVQKPVKAVTAFKADISFI 607  
QY 590 ELKSIIAAGFCVMMVHTAIBEVHIVKLLHLEKGTNRKSKPPAFAPAKGKMKVIAVLETE 649  
DB 608 DTKNIIICPGYSCVLHVHTLASEVSVTSFLHYVEKTKREKSKKPPQFQAKAGMLVSLIETS 667  
QY 650 APVCVETQDYPQLGRFTLRDQGTIIAIGKIVKIAE 685  
DB 668 APICIERFEDYKMLGRFTLRDEGKTVIAIGKIVKIAE 703

## RESULT 9

US-10-732-923-17101  
; Sequence 17101, Application US/10732923  
; Publication No. US20050108791A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923  
; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; PRIOR FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 17101  
; LENGTH: 629  
; TYPE: PRT  
; ORGANISM: Pneumocystis carinii  
US-10-732-923-17101

Query Match 45.2%; Score 1626; DB 17; Length 629;









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